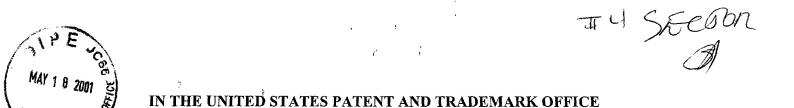
, 1



In re application of

Samir Kumar BRAHMACHARI et al.

Appln. No.: 09/820,843

Group Art Unit: Not Yet Assigned

Filed: March 30, 2001

Examiner: Not Yet Assigned

Confirmation number: 7045

For: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE

PROTEINS USEFUL AS ANTI-INFECTIVES

## STATEMENT TO SUPPORT FILING AND SUBMISSION IN ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents Washington, D.C. 20231 **Box SEQUENCE** 

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

- 1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include any new matter;
- 2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and
- 3. all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by

fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Drew Hissong

Registration No. 44,765

SUGHRUE, MION, ZINN, MACPEAK & SEAS, PLLC 2100 Pennsylvania Avenue, N.W. Washington, D.C. 20037-3213 Telephone: (202) 293-7060 Facsimile: (202) 293-7860

Date: May 18, 2001

## SEQUENCE LISTING

```
<110> Council of Scientific and Industrial Research
<120> A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEINS
USEFUL AS ANTI-INFECTIVES
<130> Q63915
<160> 118
<170> PatentIn version 3.0
<210> 1
<211> 51
<212> PRT
<213> C. jejuni
<220>
<221> misc feature
<223> highly acidic protein
<220>
<221> misc_feature
<223> gi 6967728
<400> 1
Met Ala Tyr Glu Asp Glu Glu Asp Leu Asn Tyr Asp Asp Tyr Glu Asn
                5
Glu Asp Glu Glu Tyr Pro Gln Asn His His Lys Asn Tyr Asn Tyr Asp
Asp Asp Asp Tyr Glu Tyr Asp Asp Asp Asn Asn Asp Asp Phe Tyr
Glu Met Asp
    50
<210> 2
<211> 32
<212> PRT
<213> C. jejuni
<220>
<221> misc_feature
<223> small hydrophobic protein
<220>
<221> misc_feature
<223> gi|6969129
```

```
The last finish the room and the firm of the last than the last than the last the la
```

```
<400> 2
Met Thr Met Leu Asp Ile Phe Glu Ile Ile Phe Ile Thr Thr Val Val
                5
Ile Ile Gly Phe Gly Gly Ile Val Phe Val Val Thr Lys Glu Lys Lys
<210> 3
<211> 57
<212> PRT
<213> C. jejuni
<220>
<221> misc_feature
<223> putative coiled coil protein
<220>
<221> misc_feature
<223> gi|6968493
<400> 3
Met Ser Phe Glu Glu Asn Leu Lys His Ala Asn Glu Ser Leu Glu Lys
Leu Asn Asn Gln Glu Leu Ala Leu Asp Glu Ser Val Lys Ile Tyr Lys
            20
Glu Gly Leu Glu Ser Ile Lys Lys Ala Arg Leu Glu Leu Glu Lys Ala
Lys Leu Glu Val Glu Gln Ile Asp Glu
<210> 4
<211> 542
<212> PRT
<213> C. jejuni
<220>
<221> misc_feature
<223> highly acidic protein
<220>
<221> misc feature
<223> gi 6968611
<400> 4
```

- Met Lys Ile Leu Leu Leu Asn Glu Asn Pro Val Val Ser Arg Leu Val 1 5 10 15
- Ser Leu Ser Ala Lys Lys Met Ser Tyr Asp Phe Glu Glu Leu Asn Ala 20 25 30
- Tyr Ser Glu Asn Leu Gly Asn Tyr Asp Val Ile Val Val Asp Ser Asp 35 40 45
- Thr Pro Ala Pro Leu Lys Ile Leu Lys Glu Lys Cys Asp Arg Leu Ile 50 55 60
- Phe Leu Ala Pro Arg Asn Gln Asn Val Glu Asp Ile Asp Ala Gln Ile 65 70 75 80
- Leu Gln Lys Pro Phe Leu Pro Thr Asp Phe Leu Asn Leu Leu Asn Asn 85 90 95
- Lys Asp Ala Asn Lys His Thr Ser Ile Asp Leu Pro Met Leu Ser Asn 100 105 110
- Asp Glu Asn Pro Tyr Ala Asp Ile Ser Leu Asp Leu Asp Asn Leu Asn 115 120 125
- Leu Asp Asp Leu Pro Asp Glu Asn Ser Leu Asp Ile Asn Ser Glu Gly 130 135 140
- Met Glu Asp Leu Ser Phe Asp Asp Asp Ala Gln Asp Asp Asn Ala Asn 145 150 155 160
- Lys Thr Leu Glu Thr Gln Asn Leu Glu His Glu Thr Ile Lys Glu Gln 165 170 175
- Thr Gln Glu Asp Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly
  180 185 190
- Glu Ser Glu Lys Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr 195 200 205
- Glu Pro Ser Leu Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu 210 215 220
- Ile Lys Glu Asp Asp Lys Asn Glu Glu Ile Glu Lys Gln Glu Leu Leu 225 230 235 240
- Asp Asp Ser Lys Thr Asn Thr Leu Glu Met Gln Glu Glu Leu Ser Glu 245 250 255
- Ser Gln Asp Asp Asn Ser Asn Lys Thr Leu Glu Thr Gln Asn Leu Glu 260 265 270
- His Asp Asn Leu Glu Gln Glu Thr Ile Lys Glu Gln Thr Gln Glu Asp 275 280 285

Thr Gln Ile Asp Leu Asp Leu Thr Leu Glu Asp Gly Glu Ser Glu Lys 290 295 300

Glu Asp Leu Ser Gln Glu His Thr Ala Leu Asp Thr Glu Pro Ser Leu 305 310 315 320

Asp Glu Leu Asp Asp Lys Asn Asp Glu Asp Leu Glu Asp Asn Lys Glu 325 330 335

Leu Gln Ala Asn Ile Ser Asp Phe Asp Asp Leu Pro Glu Val Glu Glu 340 345 350

Gln Glu Lys Glu Met Asp Phe Asp Asp Leu Pro Glu Asp Ala Glu Phe 355 360 365

Leu Gly Gln Ala Lys Tyr Asn Glu Glu Ser Glu Glu Asn Leu Glu Glu 370 375 380

Phe Ala Pro Val Val Glu Glu Asp Ile Gln Asp Glu Ile Asp Asp Phe 385 390 395 400

Ala Ser Asn Leu Ser Thr Gln Asp Gln Ile Lys Glu Glu Leu Ala Gln
405 410 415

Leu Asp Glu Leu Asp Tyr Gly Ile Asp Ser Asp Asn Ser Ser Lys Val 420 425 430

Leu Glu Asp Phe Lys Asp Glu Pro Ile Leu Asp Asp Lys Glu Leu Gly
435 440 445

Thr Asn Glu Glu Val Val Val Pro Asn Leu Asn Ile Ser Asp Phe
450 455 460

Asp Thr Leu Lys Glu Ser Asp Ile Gln Glu Ala Leu Gly Glu Glu Ile 465 470 475 480

Leu Glu Lys Asn Glu Glu Pro Ile Val Ser Asp Val Thr Lys Asp Asp 485 490 495

Asn Ser Glu Glu Ile Val Asn Glu Leu Ser Gln Ser Ile Ala Gly Ala 500 505 510

Ile Thr Ser Ser Ile Lys Asp Asp Thr Leu Lys Ala Ala Leu Lys Gly 515 520 525

Met Asn Met Asn Ile Asn Ile Asn Ile Ser Phe Lys Glu Asp 530 535 540

<210> 5

<211> 172

<212> PRT

<213> C. pneumoniaeCWL029

<220>

<221> misc feature

<220>

<221> misc\_feature

<223> histone like protein 2 <220> <221> misc\_feature <223> gi 4376663 <400> 5 Met Ile Gly Ala Gln Lys Lys Gln Ser Gly Lys Lys Thr Ala Ser Arg Ala Val Arg Lys Pro Ala Lys Lys Val Ala Ala Lys Arg Thr Val Lys 20 Lys Ala Thr Val Arg Lys Thr Ala Val Lys Lys Pro Ala Val Arg Lys Thr Ala Ala Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg Thr Val Arg Lys Thr Val Ala Lys Lys Pro Ala Val Lys Lys Val Ala Ala Lys Arg Val Val Lys Lys Thr Val Ala Lys Lys Thr Thr Ala Lys Arg Ala Val Arg Lys Thr Val Ala Lys Lys Pro Val Ala Arg Lys Thr Thr 110 Val Ala Lys Gly Ser Pro Lys Lys Ala Ala Ala Cys Ala Leu Ala Cys His Lys Asn His Lys His Thr Ser Ser Cys Lys Arg Val Cys Ser Ser Thr Ala Thr Arg Lys His Gly Ser Lys Ser Arg Val Arg Thr Ala His 145 150 Gly Trp Arg His Gln Leu Ile Lys Met Met Ser Arg 165 <210> 6 <211> 63 <212> PRT <213> C. trachomatis <220> <221> misc feature <223> hypothetical protein-possible frameshift with CT593

5/155

<223> gi 3522902

<400> 6

Met Phe Thr Leu Phe Leu Cys Glu His Leu Leu Thr Asn Ile Leu Ala 1 5 10 15

Ser Ser Phe Leu Ala Lys Ser Gln Gly Phe Ile Thr Leu Val Asn Leu 20 25 30

Phe His Lys Ile Pro Gly Leu Lys Val Ile Glu Ile Thr Cys Leu Ala 35 40 45

Leu Pro Leu Gly Ile His Ser Ile Ile Gly Phe Ser Tyr Leu Leu 50 55 60

<210> 7

<211> 203

<212> PRT

<213> C. trachomatis

<220>

<221> misc\_feature

<223> histone like protein 2

<220>

<221> misc\_feature

<223> gi 3328438

<400> 7

Met Asn Met Leu Gly Val Gln Lys Lys Cys Ser Thr Arg Lys Thr Ala 1 5 10 15

Ala Arg Lys Thr Val Val Arg Lys Pro Ala Ala Lys Lys Thr Ala Ala 20 25 30

Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys Thr Val Ala Arg 35 40 45

Lys Thr Val Ala Lys Lys Thr Val Ala Arg Lys Pro Val Ala Lys 50 55 60

Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Val Ala Ala Lys Lys 65 70 75 80

Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val Ala Ala Arg Lys
85 90 95

Pro Val Ala Lys Lys Ala Thr Ala Lys Lys Ala Pro Val Arg Lys Ala
100 105 110

Val Ala Lys Lys Thr Val Ala Arg Lys Thr Val Ala Lys Lys Thr Val
115 120 125

Ala Ala Arg Lys Pro Val Ala Lys Arg Val Ala Ser Thr Lys Lys Ser 130 135 140

Ser Ile Ala Val Lys Ala Gly Val Cys Met Lys Lys His Lys His Thr 145 150 155 160

Ala Ala Cys Gly Arg Val Ala Ala Ser Gly Val Lys Val Cys Ala Ser 165 170 175

Ala Ala Lys Arg Lys Thr Asn Pro Asn Arg Ser Arg Thr Ala His Ser 180 185 190

Trp Arg Gln Gln Leu Met Lys Leu Val Ala Arg

<210> 8

<211> 372

<212> PRT

<213> H. influenzae

<220>

<221> misc feature

<223> outer membrane integrity protein (tolA)

<220>

<221> misc\_feature

<223> gi | 1573353

<400> 8

Met Gln Asn Asn Arg Gln Lys Lys Gly Ile Asn Ala Phe Ala Ile Ser 1 5 10 15

Ile Leu Leu His Phe Ile Leu Phe Gly Leu Leu Ile Leu Ser Ser Leu 20 25 30

Tyr His Thr Val Glu Ile Met Gly Gly Glu Gly Glu Gly Asp Val
35 40 45

Ile Gly Ala Val Ile Val Asp Thr Gly Thr Ala Ala Gln Glu Trp Gly 50 55 60

Arg Ile Gln Gln Lys Lys Gly Gln Ala Asp Lys Gln Lys Arg Pro 65 70 75 80

Glu Pro Val Val Glu Glu Lys Pro Pro Glu Pro Asn Gln Glu Glu Ile 85 90 95

Lys His Gln Glu Val Gln Arg Gln Glu Glu Leu Lys Arg Gln Gln
100 105 110

Glu Gln Gln Arg Gln Gln Glu Ile Lys Lys Gln Gln Glu Gln Ala Arg 115 120 125

Gln Glu Ala Leu Glu Lys Gln Lys Gln Ala Glu Glu Ala Lys Ala Lys 130 135 140

Gln Ala Ala Glu Ala Ala Lys Leu Lys Ala Asp Ala Glu Ala Lys Arg 145 150 155 160

Leu Ala Ala Ala Lys Gln Ala Glu Glu Glu Ala Lys Ala Lys Ala 165 170 175

Ala Glu Ile Ala Ala Gln Lys Ala Lys Gln Glu Ala Glu Ala Lys Ala 180 185 190

Lys Leu Glu Ala Glu Ala Lys Ala Lys Ala Val Ala Glu Ala Lys Ala 195 200 205

Lys Ala Glu Ala Glu Ala Lys Ala Lys Ala Ala Glu Ala Lys Ala 210 215 220

Lys Ala Asp Ala Glu Ala Lys Ala Ala Thr Glu Ala Lys Arg Lys Ala 225 230 235 240

Asp Gln Ala Ser Leu Asp Asp Phe Leu Asn Gly Gly Asp Ile Gly Gly 245 250 255

Gly Ser Ala Ser Lys Gly Gly Asn Thr Asn Lys Gly Gly Thr Gln Gly 265 270

Ser Gly Ala Ala Leu Gly Ser Gly Asp Gly Gly Lys Val Gly Asp Gln 275 280 285

Tyr Ala Gly Val Ile Lys Lys Glu Ile Gln Arg Arg Phe Leu Lys Asp 290 295 300

Pro Asn Phe Ala Gly Lys Val Cys Arg Ile Lys Ile Gln Leu Gly Arg 305 310 315 320

Asp Gly Thr Ile Leu Gly Tyr Gln Lys Ile Ser Gly Ser Asp Asp Ile 325 330 335

Cys Ser Ala Ala Leu Ser Ala Val Ala Arg Thr Lys Lys Val Pro Ala 340 345 350

Ala Pro Ser Asp Glu Ile Tyr Glu Lys Tyr Lys Ser Pro Ile Ile Asp 355 360 365

Phe Asp Ile Arg 370

<210> 9 <211> 538 <212> PRT

<213> H. influenzae <220> <221> misc feature <223> thiamin ABC transporter, permease protein, putative <220> <221> misc feature <223> gi | 1574049 <400> 9 Met Phe Ser Leu Phe His His Pro Gln Leu Arg Pro Arg His Tyr Ala Gly Gly Val Val Ile Ser Phe Ile Ile Leu Phe Tyr Gly Gly Ala 20 Leu Ser Ser Ile Phe Ala Leu Gly Gly Glu Leu Gln Trp Arg Ala Trp Phe Thr Asp Asp Tyr Leu Gln His Leu Ile Leu Phe Ser Phe Gly Gln Ala Leu Leu Ser Thr Val Leu Ser Ile Phe Phe Gly Leu Leu Ala 70 Arg Ala Leu Phe Tyr Lys Pro Phe Leu Gly Lys Lys Trp Leu Leu Lys Leu Met Ser Leu Thr Phe Val Leu Pro Ala Leu Val Val Ile Phe Gly 100 105 Leu Ile Gly Ile Tyr Gly Ser Ser Gly Trp Leu Ala Trp Leu Ala Asn 120 Leu Phe Gly Met Ser Trp Gln Gly His Ile Tyr Gly Leu Ser Gly Ile 135 Leu Ile Ala His Leu Phe Phe Asn Ile Pro Leu Ala Ala Gln Leu Phe 145 160 Leu Gln Ser Leu Gln Ser Ile Pro Tyr Gln Gln Arg Gln Leu Ala Ala 165 170 Gln Leu Asn Leu Gln Gly Trp Gln Phe Val Lys Leu Val Glu Trp Pro 180 185 Val Phe Arg Gln Gln Cys Leu Pro Thr Phe Ser Leu Ile Phe Met Leu 195 200

9/155

Cys Phe Thr Ser Phe Thr Val Val Leu Thr Leu Gly Gly Gly Pro Gln

215

Tyr Thr Thr Leu Glu Thr Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe Asp Leu Pro Lys Ala Ala Leu Phe Ala Met Leu Gln Phe Val Phe Cys 245 Leu Ile Leu Phe Ser Leu Thr Ser Arg Phe Ser Leu Ser Asn Gln Asn Gly Leu Ser Asn Ser Asn Ile Trp Phe Glu Lys Pro Lys Ser Ala Val 280 Lys Ile Phe His Ile Leu Val Leu Leu Val Phe Val Phe Phe Leu Phe 290 295 Ser Pro Val Leu Asn Ile Leu Ile Ser Ala Leu Ser Ser Ser Asn Leu 310 Leu Thr Val Trp His Asn Ser Gln Leu Trp Arg Ala Leu Gly Tyr Ser 330 Leu Ser Ile Ala Pro Leu Ser Ala Leu Leu Ala Leu Thr Met Ala Ile 340 345 Ala Leu Leu Leu Ser Arg Arg Leu Glu Trp Leu His Tyr Gln Lys 360 Ile Ser Gln Phe Ile Ile Asn Ala Gly Met Val Ile Leu Ala Ile Pro 375 Ile Leu Val Leu Ala Met Gly Leu Phe Leu Leu Leu Gln Asp Arg Asp Phe Ser Asn Ile Asp Leu Phe Ile Ile Val Val Phe Cys Asn Ala Leu 410 Ser Ala Met Pro Phe Val Leu Arg Ile Leu Ser Ala Pro Phe His Asn 420 Asn Met Arg Tyr Tyr Glu Asn Leu Cys Asn Ser Leu Gly Ile Val Gly Trp Gln Arg Phe Tyr Leu Ile Glu Trp Lys Thr Leu Arg Ala Pro Leu 450 455 Arg Tyr Ala Phe Ala Leu Gly Leu Ala Leu Ser Leu Gly Asp Phe Thr 470 Ala Ile Ala Leu Phe Gly Asn Gln Glu Phe Thr Ser Leu Pro His Leu 490

510

Leu Tyr Gln Gln Leu Gly Asn Tyr Arg Asn Gln Asp Ala Ala Val Thr

505

```
Ala Gly Ile Leu Leu Leu Cys Gly Ile Leu Phe Ala Phe Ile His
        515
                            520
Thr Tyr Arg Asp Ala Asp Asp Leu Ser Lys
    530
<210> 10
<211> 221
<212> PRT
<213> H. influenzae
<220>
<221> misc_feature
<223> heme exporter protein B (ccmB)
<220>
<221> misc_feature
<223> gi | 1574645
<400> 10
Met Ile Phe Leu Glu Ile Ile Lys Arg Glu Leu Gln Ile Ala Met Arg
Lys Asn Ala Glu Ile Leu Asn Pro Leu Trp Phe Phe Leu Leu Val Ile
           20
Thr Leu Phe Pro Leu Val Ile Gly Pro Asp Pro Lys Leu Leu Ser Arg
Ile Ala Pro Gly Ile Ala Trp Val Ala Ala Leu Leu Ser Ala Leu Leu
                        55
Ser Phe Glu Arg Leu Phe Arg Asp Phe Ile Asp Gly Ser Leu Glu
                   70
Gln Leu Met Leu Thr Ala Gln Pro Leu Pro Met Thr Ala Leu Ala Lys
                                   90
Val Val Ala His Trp Leu Leu Thr Gly Leu Pro Leu Ile Leu Leu Ser
                               105
Pro Ile Ala Ala Leu Leu Ser Leu Glu Val Asn Ile Trp Trp Ala
                            120
Leu Val Leu Thr Leu Leu Gly Thr Pro Val Leu Ser Cys Ile Gly
                       135
Ala Ile Gly Val Ala Leu Thr Val Gly Leu Arg Lys Gly Gly Val Leu
145
                   150
                                                           160
```

175

170

Leu Ser Leu Leu Val Val Pro Leu Phe Ile Pro Val Leu Ile Phe Ala

Ser Ser Val Leu Glu Ala Ala Gly Leu Asn Val Pro Tyr Gly Gln
180 185 190

Leu Ala Ile Leu Gly Ala Met Met Val Gly Ala Val Thr Leu Ser Pro 195 200 205

Phe Ala Ile Ala Ala Ala Leu Arg Ile Ser Leu Asp Asn 210 215 220

<210> 11

<211> 788

<212> PRT

<213> H. influenzae

<220>

<221> misc feature

<223> recombination protein (rec2)

<220>

<221> misc\_feature

<223> gi|1573009

<400> 11

Met Lys Leu Asn Leu Ile Thr Leu Val Val Leu Leu Ile Val Ala Asp 1 5 10 15

Leu Thr Leu Leu Phe Leu Pro Gln Pro Leu Leu Leu Pro Trp Gln Val 20 25 30

Ala Leu Val Ile Ala Leu Val Leu Ile Phe Leu Phe Ile Phe Leu Arg 35 40 45

Arg Asn Phe Leu Val Ser Leu Ala Phe Phe Val Ala Ser Leu Gly Tyr 50 55 60

Phe His Tyr Ser Ala Leu Ser Leu Ser Gln Gln Ala Gln Asn Ile Thr 65 70 75 80

Ala Gln Lys Gln Val Val Thr Phe Lys Ile Gln Glu Ile Leu His Gln 85 90 95

Gln Asp Tyr Gln Thr Leu Ile Ala Thr Ala Thr Leu Glu Asn Asn Leu
100 105 110

Gln Glu Gln Arg Ile Phe Leu Asn Trp Lys Ala Lys Glu Val Pro Gln

Leu Ser Glu Ile Trp Gln Ala Glu Ile Ser Leu Arg Ser Leu Ser Ala 130 135 140

Arg Leu Asn Phe Gly Gly Phe Asp Arg Gln Gln Trp Tyr Phe Ser Lys

145 150 155 160

Gly Ile Thr Ala Val Gly Thr Val Lys Ser Ala Val Lys Ile Ala Asp 165 170 175

Val Ser Ser Leu Arg Ala Glu Lys Leu Gln Gln Val Lys Lys Gln Thr 180 185 190

Glu Gly Leu Ser Leu Gln Gly Leu Leu Ile Ala Leu Ala Phe Gly Glu 195 200 205

Arg Ala Trp Leu Asp Lys Thr Trp Ser Ile Tyr Gln Gln Thr Asn 210 215 220

Thr Ala His Leu Ile Ala Ile Ser Gly Leu His Ile Gly Leu Ala Met 225 230 235 240

Gly Ile Gly Phe Cys Leu Ala Arg Val Val Gln Val Phe Phe Pro Thr 245 250 255

Arg Phe Ile His Pro Tyr Phe Pro Leu Val Phe Gly Val Leu Phe Ala 260 265 270

Leu Ile Tyr Ala Tyr Leu Ala Gly Phe Ser Val Pro Thr Phe Arg Ala 275 280 285

Ile Ser Ala Leu Val Phe Val Leu Phe Ile Gln Ile Met Arg Arg His 290 295 300

Tyr Ser Pro Ile Gln Phe Phe Thr Leu Val Val Gly Phe Leu Leu Phe 305 310 315 320

Cys Asp Pro Leu Met Pro Leu Ser Val Ser Phe Trp Leu Ser Cys Gly 325 330 335

Ala Val Gly Cys Leu Leu Leu Trp Tyr Arg Tyr Val Pro Phe Ser Leu 340 345 350

Phe Gln Trp Lys Asn Arg Pro Phe Ser Pro Lys Val Arg Trp Ile Phe 355 360 365

Ser Leu Phe His Leu Gln Phe Gly Leu Leu Leu Phe Phe Thr Pro Leu 370 380

Gln Leu Phe Leu Phe Asn Gly Leu Ser Leu Ser Gly Phe Leu Ala Asn 385 390 395 400

Phe Met Ala Val Pro Ile Tyr Ser Phe Leu Leu Val Pro Leu Ile Leu 405 410 415

Phe Ala Val Phe Thr Asn Gly Thr Met Phe Ser Trp Gln Leu Ala Asn 420 425 430

Lys Leu Ala Glu Gly Ile Thr Gly Leu Ile Ser Val Phe Gln Gly Asn 435 440 445

Trp Leu Thr Val Ser Phe Asn Leu Ala Leu Gly Leu Thr Ala Leu Cys Ala Gly Ile Phe Met Leu Ile Ile Trp Asn Ile Tyr Arg Glu Pro Glu 470 475 Ile Ser Ser Ser Asn Trp Gln Ile Lys Arg Ala Lys Phe Phe Thr Leu Asn Leu Ser Lys Pro Leu Leu Lys Asn Glu Arg Ile Asn Val Leu Arg 505 Cys Ser Phe Gly Ile Ile Leu Leu Cys Phe Thr Ile Leu Leu Phe Lys 515 Gln Leu Ser Lys Pro Thr Trp Gln Val Asp Thr Leu Asp Val Gly Gln 535 Gly Leu Ala Thr Leu Ile Val Lys Asn Gly Lys Gly Ile Leu Tyr Asp 545 555 Thr Gly Ser Ser Trp Arg Gly Gly Ser Met Ala Glu Leu Glu Ile Leu 570 Pro Tyr Leu Gln Arg Glu Gly Ile Val Leu Glu Lys Leu Ile Leu Ser 585 His Asp Asp Asn Asp His Ala Gly Gly Ala Ser Thr Ile Leu Lys Ala 595 600 Tyr Pro Asn Val Glu Leu Ile Thr Pro Ser Arg Lys Asn Tyr Gly Glu Asn Tyr Arg Thr Phe Cys Thr Ala Gly Arg Asp Trp His Trp Gln Gly 635 Leu His Phe Gln Ile Leu Ser Pro His Asn Val Val Thr Arg Ala Asp 645 Asn Ser His Ser Cys Val Ile Leu Val Asp Asp Gly Lys Asn Ser Val Leu Leu Thr Gly Asp Ala Glu Ala Lys Asn Glu Gln Ile Phe Ala Arg 675 680 Thr Leu Gly Lys Ile Asp Val Leu Gln Val Gly His His Gly Ser Lys Thr Ser Thr Ser Glu Tyr Leu Leu Ser Gln Val Arg Pro Asp Val Ala 710 715

735

730

Ile Ile Ser Ser Gly Arg Trp Asn Pro Trp Lys Phe Pro His Tyr Ser

Val Met Glu Arg Leu His Arg Tyr Lys Ser Ala Val Glu Asn Thr Ala 740 745 750

Val Ser Gly Gln Val Arg Val Asn Phe Phe Gln Asp Arg Leu Glu Ile 755 760 765

Gln Gln Ala Arg Thr Lys Phe Ser Pro Trp Tyr Ala Arg Val Ile Gly
770 775 780

Leu Ser Lys Glu

<210> 12

<211> 505

<212> PRT

<213> H. pylori

<220>

<221> misc feature

<223> poly E-rich protein

<220>

<221> misc\_feature

<223> gi|2313421

<400> 12

Met Lys Met Ile Leu Phe Asn Gln Asn Pro Met Ile Thr Lys Leu Leu 1 5 10 15

Glu Ser Val Ser Lys Lys Leu Glu Leu Pro Ile Glu Asn Phe Asn His
20 25 30

Tyr Gln Glu Leu Ser Ala Arg Leu Lys Glu Asn Gln Glu Trp Leu Leu 35 40 45

Ile Ala Asp Asp Glu Cys Leu Glu Lys Leu Asp Gln Val Asp Trp Leu 50 55 60

Glu Leu Lys Glu Thr Ile Ser Gln Asn Lys Asn Ser Val Cys Met Tyr 65 70 75 80

Lys Lys Gly Asn Glu Ala Gln Pro Phe Leu Glu Gly Phe Glu Val Lys 85 90 95

Ile Lys Lys Pro Phe Leu Pro Thr Glu Met Leu Lys Val Leu Gln Lys
100 105 110

Lys Leu Gly Ser Asn Ala Ser Glu Leu Glu Pro Ser Gln Asn Leu Asp 115 120 125

Pro Thr Gln Glu Val Leu Glu Thr Asn Trp Asp Glu Leu Glu Asn Leu 130 135 140

Gly Asp Leu Glu Ala Leu Val Gln Glu Glu Pro Asn Asn Glu Glu Gln 155 Leu Leu Pro Thr Leu Asn Asp Gln Glu Glu Lys Glu Glu Val Lys Glu Thr Pro Gln Glu Glu Lys Lys Pro 200 Lys Asp Asp Glu Thr Gln Glu Gly Glu Thr Leu Lys Asp Lys Glu Val Ser Lys Glu Leu Glu Ala Pro Gln Glu Leu Glu Ile Pro Lys Glu Glu 230 Thr Gln Glu Gln Asp Pro Ile Lys Glu Glu Thr Gln Glu Asn Lys Glu 250 Glu Lys Gln Glu Lys Thr Gln Asp Ser Pro Ser Ala Gln Glu Leu Glu 260 265 Ala Met Gln Glu Leu Val Lys Glu Ile Gln Glu Asn Ser Asn Gly Gln 280 Glu Asn Lys Glu Lys Thr Gln Glu Ser Ala Glu Ile Pro Gln Asp Lys 295 Glu Ile Gln Glu Val Val Thr Glu Lys Thr Gln Ala Gln Glu Leu Glu Val Pro Lys Glu Lys Thr Gln Glu Ser Ala Glu Ala Leu Gln Glu Thr 330 Gln Ala His Glu Leu Glu Lys Gln Glu Ile Ala Glu Thr Pro Gln Asp 340 Val Glu Ile Pro Gln Ser Gln Asp Lys Glu Val Gln Glu Leu Glu Ile 360 Pro Lys Glu Glu Thr Gln Glu Asn Thr Glu Thr Pro Gln Asp Val Glu 370 375 Thr Pro Gln Glu Lys Glu Thr Gln Glu Asp His Tyr Glu Ser Ile Glu 385 Asp Ile Pro Glu Pro Val Met Ala Lys Ala Met Gly Glu Glu Leu Pro 410 Phe Leu Asn Glu Ala Val Ala Lys Ile Pro Asn Asn Glu Asn Asp Thr 420 425

```
Glu Thr Pro Lys Glu Ser Val Thr Glu Thr Ser Lys Asn Glu Asn Asn
Thr Glu Thr Pro Gln Glu Lys Glu Glu Ser Asp Lys Thr Ser Ser Pro
                       455
Leu Glu Leu Arg Leu Asn Leu Gln Asp Leu Leu Lys Ser Leu Asn Gln
                                       475
                   470
Glu Ser Leu Lys Ser Leu Leu Glu Asn Lys Thr Leu Ser Ile Lys Ile
               485
                                   490
Thr Leu Glu Asp Lys Lys Pro Asn Ala
           500
<210> 13
<211> 60
<212> PRT
<213> H. pylori
<220>
<221> misc feature
<223> histidine-rich, metal binding polypeptide (hpn)
<220>
<221> misc_feature
<223> gi 2314604
<400> 13
Met Ala His His Glu Glu Gln His Gly Gly His His His His His His
                                   10
His Thr His His His Tyr His Gly Glu His His His His His
His Ser Ser His His Glu Glu Gly Cys Cys Ser Thr Ser Asp Ser His
His Gln Glu Glu Cys Cys His Gly His His Glu
<210> 14
<211> 72
<212> PRT
<213> H. pylori
<220>
<221> misc feature
<223> histidine and glutamine-rich protein
```

<220>

<221> misc feature <223> gi 2314605 <400> 14 Met Ala His His Glu Gln Gln Gln Gln Gln Ala Asn Ser Gln His 5 His His His His Ala His His His Tyr Tyr Gly Glu His 25 His His Asn Ala Gln Gln His Ala Glu Gln Gln Ala Glu Gln Gln 40 Ala Gln Gln Gln Gln Gln Gln Ala His Gln Gln Gln Gln Lys 50 Ala Gln Gln Asn Gln Gln Tyr <210> 15 <211> 1139 <212> PRT <213> M. genitalium <220> <221> misc feature <223> cytadherence-accessory protein <220> <221> misc\_feature <223> gi | 1046012 <400> 15 Met Ala Lys Asn Lys Gln Ser Val Phe Glu Glu Lys Asn Tyr Thr Gln Thr Glu Pro Glu Asn Ile Phe Gly Asp Leu Tyr Asp Gly Lys Ser Thr Val Glu Glu Asp Pro Asn Ile Lys Val Ala Tyr Asp Ala Asp Gly Asn Gly Tyr Tyr Ile Ala Phe Asn Lys Glu Thr Gly Val Tyr Tyr Asp Pro 55 Tyr Gly Asp Thr Glu Tyr Asp Ile Ser Gln Leu Phe Asp Glu Asn Gly 65 70

90

Asn Pro Phe Val Phe Asp Glu Lys Gln Glu Glu Asn Asp Tyr Leu Lys

Tyr Val Gly Asn Pro Asp Tyr Gly Ser Tyr Asp Glu Asn Gly Glu Trp 100 105 110

Val Trp Ser Gly Tyr Phe Glu Asn Asp Gln Trp Ile Ser Thr Lys Glu 115 120 125

Ser Gln Pro Thr Asp Glu Asn Tyr Gly Phe Asp Ser Asp Leu Pro Pro 130 135 140

Glu Val Lys Gln Pro Glu Ser Val Glu Asp Asn Tyr Gly Phe Asp Asn 145 150 155 160

Asp Leu Pro Pro Glu Val Lys Gln Pro Glu Ser Val Glu Asp Asn Tyr 165 170 175

Gly Phe Asp Asn Asp Leu Pro Pro Glu Val Lys Gln Pro Glu Ser Val 180 185 190

Val Asp Gln Pro Ser Ser Asp Asp Tyr Phe Ala Lys Gln Pro Thr Asp 195 200 205

Glu Asn Tyr Gly Phe Asp Asn Asp Leu Pro Pro Glu Val Lys Gln Pro 210 215 220

Glu Ser Val Val Asp Gln Pro Ser Ser Asp Asp His Phe Ala Lys Gln 225 230 235 240

Pro Glu Ser Thr Thr Asp Ser Tyr Ser Phe Asp Ser Asp Leu Pro Gln
245 250 255

Pro Thr Leu Asp Gln Pro Ser Leu Asp Asp His Val Gln Tyr Asn Phe 260 265 270

Asp His His Glu Glu Leu Lys Pro Val Ala Glu Glu Gln Asn Asn Tyr 275 280 285

Gln Val Gly Phe Asp Gln Val Gln Ala Asn Leu Asp Asn Asn Glu Glu 290 295 300

Ile Gln Pro Thr Ala Glu Lys Lys Val Thr Thr Asp Phe Glu Ser Lys 305 310 315 320

Gln Ala Gln Val Val Asp Ser Tyr Gln Leu Pro Ile Asp Thr Asp Gln 325 330 335

Gln Asp Gln Thr Thr Phe Ser Ser Phe Glu Thr Gln Pro Thr Val 340 345 350

Glu Gln Phe Asp Gln Val Asn Ser Glu Val Asn Asp Gln Phe Lys Pro 355 360 365

Glu Ile Thr Lys Glu Pro Val Leu Glu Ser Ser Phe Asn Lys Gln Asp 370 375 380

Val Val Glu Thr Ser Asp Leu Asn Ser Glu Ser Asn Leu Tyr Ser Glu 385 390 Asn Asn Lys Asp Ala Thr Asn Asn Asp Ser Leu Asn Ser Glu Phe Ile 410 Gln Leu Asn Ser Asn Ser Glu Thr Ala Ser Asp Asp Val His Tyr Glu Ser Lys Ser Glu Pro Ile His Asp Tyr Lys Phe Gly Ser Asp Leu Ser 440 435 Gln Ser Asn Ser Asn Ser Leu Glu Ser Glu Pro Val Lys Phe Asn 455 Ser Glu Thr Ala Pro Asp Ala His Phe Glu Ser Gln Ser Glu Pro Val 465 470 475 Asp Gln Val Gln Tyr Asp Ile Tyr Gln Asn Glu Glu Leu Lys Pro Thr 490 Leu Asp Gln Pro Ser Ser Asp Asp Tyr Phe Ala Lys Gln Pro Thr Asp 505 Glu Asn Tyr Gly Phe Asp Asn Asp Leu Pro Pro Glu Val Lys Gln Pro 515 Glu Ser Val Val Asp Gln Pro Ser Ser Asp Asp His Phe Ala Lys Gln Pro Glu Ser Thr Thr Asp Ser Tyr Ser Phe Asp Ser Asp Leu Pro Gln 545 550 555 Pro Thr Leu Asp Gln Pro Ser Leu Asp Asp His Val Gln Tyr Asn Phe 570 Asp His His Glu Glu Leu Lys Pro Val Ala Glu Glu Gln Asn Asn Tyr 585 Gln Val Gly Phe Asp Gln Val Gln Ala Asn Leu Asp Asn Asn Glu Glu 595 600 Ile Gln Pro Thr Ala Glu Lys Glu Val Thr Thr Asp Phe Glu Ser Lys Gln Ala Gln Val Val Asp Ser Tyr Gln Leu Pro Ile Asp Thr Asp Gln 625 630 Gln Asp Gln Thr Thr Phe Ser Ser Phe Glu Thr Gln Pro Thr Val 650 Glu Gln Phe Asp Gln Val Asn Ser Glu Val Asn Asp Gln Phe Lys Pro 665 Glu Ile Thr Lys Glu Pro Val Leu Glu Ser Ser Phe Asn Lys Gln Asp

680 685 675 Val Val Glu Thr Ser Asn Tyr Thr Asn Asn Leu Gln Lys Phe Asp Ile 690 695 Gln Ser Asp Asn Lys Ile Thr Ile Thr Thr Lys Lys Ser Ser Pro Gln 710 Ile Pro Thr Thr Leu Pro Ile Ser Phe Val Ser Asn Arg Ile Glu Tyr 730 725 Lys Pro Val Glu Thr Leu Ala Leu Asp Asn Lys Glu Ser Gln Gln Glu 740 745 Gln Ile Thr Ile Asn Ser Ile Thr Glu Asp Ser Lys Thr Leu Ala Lys 760 Thr Leu Ser Val Gln Leu Gln Gln Ile Asn Ser Leu Asn Asn Gln Ser Ile Val Thr Ser Glu Ser Val Arg Leu Asp Lys Lys Asp Asp Gln Leu 790 Thr Ile Asn Thr Val Asn Ser Glu Asp Gln Gln Pro Lys Ile Glu Val 805 810

Phe Val Lys Ala Lys Glu Pro Val Glu Glu His Ser Ile Thr Gln Asn 820 825 830

Lys Gln Ser Val Glu Asp Lys Ser Glu Leu Asp Asn Phe Asn Lys Lys 835 840 845

Ser Asp Leu Tyr Lys Ile Ile Ser Glu Leu Lys Arg Gly Glu Leu Asn 850 860

Pro Thr Ile Asn Phe Asp Ala Ile Phe Gln Met Asn Asp Tyr Gln Met 865 870 875 880

Ser Val Lys Gln Ser Phe Ile His Leu Asn Asp Phe Val Thr Asn Tyr 885 890 895

Lys Asn Gln Ile Ser Glu Arg Tyr Leu Ile Ile Lys Lys Glu Leu Gln 900 905 910

Ser Glu Leu Ser Arg Leu Ile Asp Gln Asn Glu Asn Leu Asn Val Gln 915 920 925

Phe Asn Asn Ala Lys Asn Leu Thr Thr Leu Gln Lys Glu Glu Met Ile

Arg Ser Leu Ala Ser Asp Phe Ala Ile Ala Tyr Lys Pro Ser Asn Ser 945 950 955 960

Tyr Glu Gln Leu Gln Lys Ser Gly Glu Ile Met Arg His Val Gln Arg 965 970 975 Ala Ile Thr Glu Asn Glu Lys Lys Ile Glu Ser Ile Gln Gly Ser Leu 980 985 990

Lys Gln Leu Lys Thr Val Tyr Asn Ser Cys Cys Glu Thr Ile Met Asn 995 1000 1005

Asn Ile Asn Lys Leu Asp Asn Thr Leu Arg Phe Ala Lys Lys Glu 1010 1015 1020

Lys Asp Pro Leu Leu Ser Asn Phe Asp Ser Val Thr Asp Asn 1025 1030 1035

Gly Leu Val Glu Pro Asn Gln Leu Met Asp Asp Leu Ile Asp Phe 1040 1045 1050

Ser Asn Thr Phe Asp Asn Ile Ser Asn Glu Gln Leu Asp Asp Phe 1055 1060 1065

Ile Tyr Glu Asn Met Asp Arg Asn Ile Asp Phe Glu Phe Glu Gly 1070 1075 1080

Phe Asn Asn Asp Phe Val Asp Ile Asp Ala Lys Val Met Asp Ser 1085 1090 1095

Pro Asp Arg Thr Ser Asn Phe Ser Ser Leu Leu Asp Glu Asp Leu 1115 1120 1125

Phe Glu Ser Ser Gly Asp Phe Ser Leu Asp Tyr 1130 1135

<210> 16

<211> 1616

<212> PRT

<213> M. genitalium

<220>

<221> misc\_feature

<223> cytadherence-accessory protein

<220>

<221> misc\_feature

<223> gi|1046097

<400> 16

Met Pro Lys Thr Thr Lys Asn Lys Asn Lys Asn Thr Thr Pro Lys Ser 1 10 15

Lys Thr Lys Lys Tyr Leu Glu Ser Ala Asn Lys Lys Ser Val Thr Lys

20	25	30

Pro	Lys	Lys 35	Glu	Gln	Asp	Lys	Val 40	Glu	Asn	Leu	Phe	Asp 45	Gln	Pro	Phe
Leu	Gly 50	Glu	Ile	Lys	Lys	Asn 55	Ile	Leu	Lys	Lys	Thr 60	Lys	Ser	Phe	Asn
Ser 65	Lys	Lys	Lys	Glu	Thr 70	Val	Lys	Ser	Lys	Ser 75	Lys	Ser	Pro	Ile	Asp 80
Phe	Phe	Asp	Glu	Thr 85	Lys	Arg	Gly	Val	Phe 90	Ile	Val	Pro	Pro	Glu 95	Thr
Asp	Ile	Leu	Ser 100	Arg	Arg	Glu	Leu	Asn 105	Gln	Lys	Thr	Val	Val 110	Asn	Thr
Val	Pro	Asn 115	Gln	Thr	Ser	Ser	Tyr 120	Pro	Thr	Ile	Asn	Glu 125	Asn	Lys	Leu
Val	Glu 130	Leu	Asn	Asn	Gln	Pro 135	Glu	Thr	Lys	Val	Leu 140	Glu	Thr	Lys	Lys
Asp 145	Ser	Phe	Thr	Thr	Thr 150	Ile	Arg	Glu	Lys	Lys 155	Leu	Asn	Pro	Glu	Asp 160
Ser	Gln	Ala	Phe	Trp 165	Tyr	Ile	Phe	Val	Gly 170	Asp	Arg	Lys	Tyr	Gly 175	Phe
Trp	Lys	Asn	His 180	Thr	Trp	Val	Trp	Leu 185	Gly	Tyr	Phe	Asp	Gln 190	Leu	Gln
Arg	Trp	Asn 195	Tyr	Phe	Lys	Val	Ile 200	Glu	Thr	Val	Glu	Val 205	Pro	Gln	Glu
His	Ala 210	Ala	Phe	Ile	Lys	Gln 215	Arg	Pro	Ala	Asp	Ile 220	Asp	Phe	Trp	Arg
Pro 225	Leu	Val	Gly	Asn	Pro 230	Asn	Tyr	Gly	Phe	Val 235	Gln	Asn	Asn	Thr	Trp 240
Ile	Trp	Lys	Gly	Phe 245	Phe	Asp	Lys	Lys	Leu 250	Asn	Trp	Ile	Pro	Asp 255	Pro
Val	Arg	Phe	Thr 260	Glu	Glu	Ala	Leu	Gly 265	His	Thr	Asp	Ser	Leu 270	Val	Asp
Glu	Ile	Glu 275	Lys	Lys	Thr	Ile	Ser 280	Glu	Gln	Pro	Tyr	Trp 285	Glu	Gln	Glu
Asn	Asp 290	Ile	Val	Val	Thr	Val 295	Phe	Asn	Thr	Lys	Ser 300	Leu	Ala	Ser	Ser
Leu 305	Glu	Asn	Glu	Leu	Leu 310	Leu	Glu	Asn	Ser	Ser 315	Glu	Glu	Gln	Pro	Val 320

Ile Glu Glu Val Lys Pro Arg Arg Asn Glu Val Ile Phe Arg Asn Pro Val Thr Lys Leu His Phe Glu Lys Glu Lys Phe Glu Phe Leu Asn Pro 345 Val Lys Glu Thr Asn Glu Thr Ile Pro Leu Ile Glu Ile Val Lys Glu 360 Glu Val Lys Val Glu Ser Glu Val Glu Ala Pro Val Glu Ile Glu Pro Glu Ala Ala Cys Glu Pro Glu Thr Thr Ile Pro Glu Val Glu Thr Val 390 Phe Val Tyr Glu Asp Asp Leu Lys Gly Leu Asp Ser Asn Gln Thr Gln 410 Ala Gly Asn Val Pro Glu Val Glu Thr Val Phe Val Tyr Glu Asp Asp 425 Leu Lys Gly Leu Asp Ser Ile Ile Lys Asp Asp Gln Gln His Asp Glu 440 435 Ile Ala Lys His Val Glu His Leu Ser Gln Asp Tyr Ser Lys Glu Ile 455 Lys Asp Ser Ala Lys Ala Asp Leu Ser Asn Ile Ser Asp Asp Ile Asp 475 465 470 Ser Val Trp Lys Glu Phe Gly Ser Phe Thr Asp Glu Thr Gln Lys Ser Val Glu Glu Lys Ser Gln Val Asp Glu Ile Ile Leu Asp Ala Asn Asn 505 Asp Phe Ile Asn Glu Ser Leu Phe Arg Asp Glu Val Val Asn Asn Ile 515 520 Asp Ser Gln Ile Asn Glu Thr Val Ser Glu Gln Gln Phe Glu Pro Thr 535 Tyr Ser Val Asn Glu Phe Gln Glu Phe Ser Glu Pro Val Val Ser 555 550 545 Asp Glu Lys Ile Lys Glu Thr Asn Ser Asp Glu Ser Val Asn Thr Asp 570 565 Leu Thr Ala Leu Phe Ser Glu Lys Leu Val Asn Glu Val Leu Leu Thr 585

605

Asn Glu Tyr Val Asp Val Asn Ala Pro Phe Ser Thr Glu Thr Glu Val

600

Lys Val Ser Ser Glu Leu Pro Lys Ser Glu Leu Val Asp Glu Ile Thr 610 Phe Ile Asn Asn Asp Pro Lys Pro Gln Glu Gly Leu Glu Tyr Lys Val 630 Asp Phe Leu Glu Thr Glu Pro Lys Ser Leu Phe Asp Glu Lys Thr Thr 650 Ile Val Val Glu Ser Glu Pro Pro Phe Ile Gln Pro Asp Leu Ser Leu 665 Glu Leu Asp Ser Val Asn Asp Val Asp Lys Ser Leu Glu Thr Lys Thr 680 Thr Ser Val Glu Leu Asn His Glu Glu Ile Gly Asn Glu Phe Ile Asn 690 695 Leu Asp Val Ser Glu Lys Glu Val Gln Glu Gln Pro Thr Thr Gln Leu 710 Glu Thr Asp Ser Glu Phe Val Leu Pro Thr Tyr Gln Ile Val Glu Asp 725 730 Ser Phe Thr Glu Ser Ala Glu Thr Pro Asn Glu Phe Ser Ser Glu Gln Lys Asp Thr Leu Glu Phe Ile Ser Gln Thr Gln Glu Val Glu Thr Ser 760 Glu Ser Asn Val Pro Thr Val Glu Glu Glu Thr Lys Leu Phe Glu His 770 775 780 Gln Asp Glu Asn Asn Leu Phe Thr Pro Leu Pro Leu Asp Leu Thr Glu 790 795 Ile Ile Glu Ser Asn Ala Leu Phe Asp Ser Lys Pro Asp Glu Lys Glu 805 810 Ser Ser Asp Ser Glu Leu Gln Pro Thr Phe Lys Glu Ile Lys Leu Asp 820 825 Ser Thr Val Glu Val Pro Gln Glu Ser Ser Gln Val Glu Ala Thr Phe Asp Thr Val Gln Pro Glu Ala Val Phe Asp Glu Ile Lys Thr Gln Glu 850 855 Leu Gln Pro Glu Ala Thr Thr Glu Val Val Phe Asp Asp His Phe Gln 870 Pro Asp Val Gln Pro Glu Gln Thr Pro Gln Glu Ala Lys Phe Asp Ser 890 Pro Val Glu Ile Pro Gln Glu Ser Ser Gln Ala Glu Phe His Ala Glu

900 905 910

Gln Ile Ser Asp Glu Ile Lys Leu Glu Glu Lys Thr Glu Ala Val Phe 915 920 925

Asp His Gln Gln Leu Glu Asn Gln Ser Glu Glu Thr Val Val Thr Pro 930 935 940

Thr Glu Val Thr Ala Phe Glu Pro Glu Thr Ile Glu Thr Gln Leu Glu 945 950 955 960

Pro Ser Ser Glu Asp Gln Pro Ser Glu Pro Ala Leu Asp Gln Asn His
965 970 975

Pro Glu Ile Val Thr Ala Glu Val Glu Gln Ile Phe Asp Gly Thr Lys 980 985 990

Leu Glu Asp Leu Lys Leu Glu Glu Ala Asn Phe Asp Asn Val Glu Asn 995 1000 1005

Asn Glu Val Gln Pro Lys Glu Thr Glu Ala Glu Ile Thr Phe Asp 1010 1015 1020

Glu Thr Lys Glu Leu Gln Gln Glu Thr Ser Ser Glu Pro Leu Ser 1025 1030 1035

Thr Glu Glu Leu Lys Ser Glu Ala Thr Phe Asp Asn Val Ser Glu 1040 1045 1050

Ala Glu Ser Glu Ala Val Phe Glu Lys Pro Gln Leu Glu Thr Gln 1055 1060 1065

Thr Glu Lys Ile Leu Glu Glu Glu Pro Lys Ser Glu Pro Val Asp 1070 1075 1080

Gln Leu Ile Thr Glu Ala Ser Phe Asp Thr Val Lys His Glu Ala 1085 1090 1095

Val Phe Asp Lys Asn Gln Thr Gln Thr Glu Gly Leu Glu Glu Pro 1100 1105 1110

Gln Val Ser Ser Glu Ala Glu Val Val Asp Gln Thr Thr Asp 1115 1120 1125

Thr Val Gly Glu Pro Glu Ala Val Phe Asp Val Gln Pro Glu Lys 1130 1135 1140

Thr Thr Glu Val Lys Phe Asp Asp Val Glu Asn Gln Gln Lys Val 1145 1150 1155

Ile Ser Glu Pro Gln Val Glu Gln Gln Pro Gly Glu Ala Val Phe 1160 1165 1170

Glu Pro Ser Ala Glu Ala Lys Phe Asp Ser Pro Val Glu Ser Val 1175 1180 1185

Gln Asp Ser Gln Pro Glu Pro Val Leu Glu Glu Val Gln Thr Gln 1190 1195 Pro Glu Ile Gln Pro Val Glu Ser Gln Pro Glu Ala Thr Phe Asp 1205 1210 Thr Val Gln Pro Glu Gln Thr Pro Gln Glu Ala Lys Phe Asp Ser 1220 1225 Pro Val Glu Thr Val Glu Gln Pro Glu Phe Ser Ser Glu Pro Thr 1240 Gln Gln His Val Glu Ser Glu Ala Ser Phe Asp Glu Pro Asn Tyr 1250 1255 Asp Phe Asp Glu Pro Asn Tyr Asp Phe Asp Gln Pro Ser Tyr Asp 1270 Ser Asp Leu Gln Pro Ser Glu Pro Gln Tyr Asp Val Asp Glu Pro 1285 Asn Tyr Asp Phe Asp Glu Pro Asn Tyr Glu Ile Glu Ser Lys Pro 1295 1300 Ser Glu Pro Gln Phe Glu Pro Gln Val Glu Gln Gln Pro Gly Glu 1315 1310 Ala Val Phe Glu Pro Ser Ala Glu Ala Lys Phe Asp Ser Pro Val 1325 1330 1335 Glu Ser Val Gln Asp Ser Gln Pro Glu Pro Leu Leu Glu Glu Val -1345 1340 Gln Thr Gln Pro Glu Ile Gln Pro Val Glu Ser Gln Pro Glu Ala 1360 Thr Phe Asp Thr Val Gln Pro Glu Gln Thr Pro Gln Glu Ala Lys 1375 1370 Phe Asp Ser Pro Val Glu Thr Ile Gln Glu Pro Gln Val Ser Ser 1390 Glu Pro Glu Val Val Gln Pro Asn Phe Glu Glu Arg Lys Pro 1400 1405 1410 Glu Thr Val Leu Glu Glu Pro Gln Ala Asp Glu Ile Gln Pro Glu 1415 1420 Ala Ser Glu Glu Ser Leu Asp Trp Glu Leu Leu Val Gly Asn 1435 Asn Ser Tyr Gly His Tyr Glu Pro Asp Gly Glu Trp Val Trp Ala 1450 1445

```
Gly Phe Phe Gly Asp Asp Gln Lys Trp Asn Lys Asp Ala Thr Val
    1460
                        1465
                                             1470
Lys Trp Ala Arg Glu Arg Asp Tyr Leu Pro Leu Ile Gly Asp Glu
    1475
                        1480
                                             1485
Val Tyr Gly Arg Tyr Asn Asn Lys Gly Glu Trp Ile Trp Tyr Gly
                        1495
Phe Tyr Asp Glu Ser Gly Asp Trp Val Leu Val Asp Glu Gln Trp
    1505
                        1510
                                             1515
Lys Asn Arg Gln Pro Arg Ile Asn Glu Ala Pro Lys Phe Trp Glu
                        1525
Lys Leu Ile Gly Asn Glu Glu Tyr Gly Tyr Tyr Glu Asp Asn Glu
    1535
                        1540
                                             1545
Trp Asn Trp Tyr Asp Gly Glu Phe Asp Ser Glu Gly Asn Trp Leu
                        1555
Val Phe Gln Ser Glu Glu Thr Glu Asn Leu Asn Glu Asp Ile Thr
                        1570
Lys Asp Ile Pro Ala Leu Glu Gly Tyr Asp Ile Asp Ser Ile Asp
   1580
                        1585
Ala Asp Glu Trp Leu Ser Gln Phe Ser Ala Asp Asp Ala Lys Asp
   1595
                        1600
                                             1605
Val Phe Gly Ser Asn Asp Lys Lys
   1610
                        1615
<210> 17
<211> 274
<212> PRT
<213> M. pneumoniae
<220>
<221> misc_feature
<223> 30K adhesin-related protein
<220>
<221> misc feature
<223> gi 1674069
<400> 17
Met Lys Leu Pro Pro Arg Arg Lys Leu Lys Leu Phe Leu Leu Ala Trp
```

Met Leu Val Leu Phe Ser Ala Leu Ile Val Leu Ala Thr Leu Ile Leu 20 25 30

Val Gln His Asn Asn Thr Glu Leu Thr Glu Val Lys Ser Glu Leu Ser
35 40 45

Pro Leu Asn Val Val Leu His Ala Glu Glu Asp Thr Val Gln Ile Gln 50 55 60

Gly Lys Pro Ile Thr Glu Gln Ala Trp Phe Ile Pro Thr Val Ala Gly 65 70 75 80

Cys Phe Gly Phe Ser Ala Leu Ala Ile Ile Leu Gly Leu Ala Ile Gly 85 90 95

Leu Pro Ile Val Lys Arg Lys Glu Lys Arg Leu Leu Glu Glu Lys Glu
100 105 110

Arg Gln Glu Gln Leu Ala Glu Gln Leu Gln Arg Ile Ser Ala Gln Gln
115 120 125

Glu Glu Gln Gln Ala Leu Glu Gln Gln Ala Ala Glu Ala His Ala 130 135 140

Glu Ala Glu Val Glu Pro Ala Pro Gln Pro Val Pro Val Pro Pro Gln 145 150 155 160

Pro Gln Val Gln Ile Asn Phe Gly Pro Arg Thr Gly Phe Pro Pro Gln 165 170 175

Pro Gly Met Ala Pro Arg Pro Gly Met Pro Pro His Pro Gly Met Ala 180 185 190

Pro Arg Pro Gly Phe Pro Pro Gln Pro Gly Met Ala Pro Arg Pro Gly 195 200 205

Met Pro Pro His Pro Gly Met Ala Pro Arg Pro Gly Phe Pro Pro Gln 210 215 220

Pro Gly Met Ala Pro Arg Pro Gly Met Pro Pro His Pro Gly Met Ala 225 230 235 240

Pro Arg Pro Gly Phe Pro Pro Gln Pro Gly Met Ala Pro Arg Pro Gly 245 250 255

Met Gln Pro Pro Arg Pro Gly Met Pro Pro Gln Pro Gly Phe Pro Pro 260 265 270

Lys Arg

<210> 18

<211> 256

<212> PRT

<213> M. tuberculosis

<220>

225

```
<221> misc feature
<223> PE PGRS
<220>
<221> misc feature
      gi | 3261822
<223>
<400> 18
Met Ile Gly Asp Gly Ala Asn Gly Gly Pro Gly Gln Pro Gly Gly Pro
Gly Gly Leu Leu Tyr Gly Asn Gly Gly His Gly Gly Ala Gly Ala Ala
Gly Gln Asp Arg Gly Ala Gly Asn Ser Ala Gly Leu Ile Gly Asn Gly
Gly Ala Gly Gly Ala Gly Gly Asn Gly Gly Ile Gly Gly Ala Gly Ala
Pro Gly Gly Leu Gly Gly Asp Gly Gly Lys Gly Phe Ala Asp Glu
Phe Thr Gly Gly Phe Ala Gln Gly Gly Arg Gly Gly Phe Gly Gly Asn
Gly Asn Thr Gly Ala Ser Gly Gly Met Gly Gly Ala Gly Gly Ala Gly
                               105
Gly Ala Gly Gly Ala Gly Leu Leu Ile Gly Asp Gly Gly Ala Gly
Gly Ala Gly Gly Ile Gly Gly Ala Gly Gly Val Gly Gly Gly Gly
                       135
    130
Ala Gly Gly Thr Gly Gly Gly Val Ala Ser Ala Phe Gly Gly
Asn Ala Phe Gly Gly Arg Gly Gly Asp Gly Gly Asp Gly Asp Gly
Gly Thr Gly Gly Ala Gly Gly Ala Arg Gly Ala Gly Gly Ala Gly Gly
            180
Ala Gly Gly Trp Leu Ser Gly His Ser Gly Ala His Gly Ala Met Gly
                           200
Ser Gly Gly Glu Gly Gly Ala Gly Gly Gly Gly Ala Arg Gly Glu
    210
Ala Gly Ala Gly Gly Gly Thr Ser Thr Gly Thr Asn Pro Gly Lys Ala
```

230

```
Gly Ala Pro Gly Thr Gln Gly Asp Ser Gly Asp Pro Gly Pro Pro Gly
                                    250
<210> 19
<211> 484
<212>
       PRT
<213> M. tuberculosis
<220>
<221> misc feature
<223> PE PGRS
<220>
<221> misc_feature
<223> gi 2894254
<400> 19
Ala Gln Ala Ser Pro Ala Ala His Gly Gly Ser Gly Gly Ala Gly Gly
Asn Gly Gly Ala Gly Ser Ala Gly Asn Gly Gly Ala Gly Gly Ala Gly
Gly Asn Gly Gly Ala Gly Gly Asn Gly Gly Gly Asp Ala Gly Asn
Ala Gly Ser Gly Gly Asn Gly Gly Lys Gly Gly Asp Gly Val Gly Pro
Gly Ser Thr Gly Gly Ala Gly Gly Lys Gly Gly Ala Gly Ala Asn Gly
Gly Ser Ser Asn Gly Asn Ala Arg Gly Gly Asn Ala Gly Asn Gly Gly
His Gly Gly Ala Gly Gly Ser Gly Asp Thr Gly Gly Ala Gly Gly Ala
            100
Gly Gly Gln Gly Gly Phe Gly Gly Thr Gly Gly Ser Gly Ser Gly Ile
                            120
Gly Gly Gly Ala Gly Gly Asn Gly Gly Asn Gly Gly Ala Gly Gly Thr
    130
                        135
Gly Val Val Leu Gly Gly Lys Gly Gly Asp Gly Asp Gly Asp His
145
Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly Ala Gly
Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly Ser Gly
```

 Cly
 Lys
 Gly
 Ala
 A

Gly Gly Ser Gly Phe Phe Gly Gly Lys Gly Gly Phe Gly Gly Asp Gly 325 330 335

Gly Gln Gly Gly Pro Asn Gly Gly Gly Thr Val Gly Thr Val Ala Gly 340 350

Gly Gly Asn Gly Gly Val Gly Gly Arg Gly Gly Asp Gly Val Phe 355 360 365

Ala Gly Ala Gly Gly Gln Gly Gly Leu Gly Gly Gln Gly Gly Asn Gly 370 375 380

Gly Gly Ser Thr Gly Gly Asn Gly Gly Leu Gly Gly Ala Gly Gly Gly 385 390 395 400

Gly Gly Asn Ala Pro Asp Gly Gly Phe Gly Gly Asn Gly Gly Lys Gly
405
410
415

Gly Gln Gly Gly Gly Gly Gly Thr Gln Ser Ala Thr Gly Leu Gly
420 425 430

Gly Asp Gly Gly Asp Gly Gly Asp Gly Gly Asn Gly Gly Asn Ser Gly
435
440

Ala Lys Ala Gly Gly Ala Gly Gly Lys Gly Gln Ala Gly Gln Pro Asn 450 455 460

Ser Gly Thr Glu Pro Gly Phe Gly Gly Asp Gly Gly Leu Gly Gly Ala 465 470 475 480 Gly Ala Thr Pro

```
<210> 20
```

<211> 1079

<212> PRT

<213> M. tuberculosis

<220>

<221> misc feature

<223> PE PGRS

<220>

<221> misc feature

<223> gi|2924449

<400> 20

Pro Gln Gly Ala Asp Gly Asn Ala Gly Asn Gly Gly Asp Gly Val
1 5 10 15

Gly Gly Asn Gly Gly Asn Gly Ala Asp Asn Thr Thr Ala Ala Ala 20 25 30

Gly Thr Thr Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Thr Gly 35 40 45

Gly Thr Gly Gly Ala Ala Gly Thr Gly Thr Gly Gln Gln Gly Asn 50 55 60

Gly Gly Asn Gly Gly Asn Gly Gly Thr Gly Gly Lys Gly Gly Thr Gly 65 70 75 80

Gly Asp Gly Ala Leu Ala Gly Ser Ser Gly Gly Ala Gly Gly Lys Gly 85 90 95

Gly Asn Gly Gly Asp Ala Gly Lys Ala Gly Thr Gly Ser Ala Pro Gly
100 105 110

Thr Ala Gly Thr Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ile 115 120 125

Gly Ala Ala Gly Thr Thr Gly Pro Val Gly Thr Gly Ala Ser Gly Gly 130 135 140

Thr Gly Gly Ser Gly Gly Ala Gly Gly Thr Gly Gly Asp Gly Gly Ala 145 150 155 160

Ala Asn Gly Gly Thr Ala Gly Ala Gly Gly Ala Gly Gly Asn Gly Gly
165 170 175

Lys Gly Gly Asp Gly Gly Ala Gly Val Thr Ser Ser Thr Ala Gly Asn

465

180 185 190

Ser Gly Gly Ala Gly Gly Ser Gly Gly Lys Gly Gly Asp Ala Gly Ala 195 200 Gly Gly Ala Gly Ala Thr Pro Gly Ala Asn Gly Ile Ala Gly Asn Gly Gly Asp Gly Gly Asp Gly Ala Ala Gly Ala Val Gly Ile Ser Gly Ala 230 Thr Gly Ala Gly Asp Gly Gly His Gly Gly Thr Gly Ala Ala Gly Gly Asn Gly Gly Thr Gly Gly Ala Gly Gly Ser Gly Ile Asp Gly Val Gly 265 Gly Gly Thr Gly Gly Thr Gly Gly Asn Gly Asn Gly Ala Ile Gly Gly Ala Gly Gly Asp Ala Gly Gly Ser Gly Asn Ser Gly Gly Asn Gly Gly Ile Gly Gly Lys Gly Gly Asn Ala Gly Ala Gly Gly Ala Ala Gly Ser Asn Gly Gly Thr Val Gly Ala Asn Gly Thr Gly Gly Asp Gly Gly Asn Gly Gly Ala Ala Gly Ala Ala Thr Ala Gly Ser Asn Gly Gly Ala 345 Gly Thr Gly Ser Ala Gly Gly Asn Gly Gly Thr Gly Gly Arg Gly Gly Ser Gly Gly Ala Gly Gly Asp Gly Ile Gly Gly Val Gly Gly Lys 370 Gly Gly Asn Gly Ala Asp Gly Glu Val Gly Gly Ala Gly Gly Ala Gly Gly Ser Gly Pro Asn Thr Ser Pro Gly Gly Asn Gly Gly Gln Gly Gly Gln Gly Gly Ser Gly Gly Ala Gly Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Gly Ala Asn Gly Thr Ala Gly Asn Gly Gly Gln Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Ala Ala Ser Ser Ala Thr Asn Gly Gly 450

475

Ser Gly Gly Ala Gly Gly Thr Gly Gly Asp Gly Gly Ser Gly Gly Ala

755

Gly Gly Thr Gly Gly Ala Gly Gly Thr Gly Gly Ala Ala Gly Asp Gly 490 Gly Gln Gly Gln Gly Gly Ala Gly Gly Gly Ala Gly Gln Gly 500 Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Asn Gly Gly Asn Ile Thr Gly Gly Thr Ala Gly Thr Ala Gly Ala Ala Gly Asn Gly Gly Ala Ala Gly Lys Gly Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Thr Gly Gly Gln Gly Gly Ala Gly Gly Asp Gly Gly Ala Gly Gly Thr Gly Gly Asp Arg Thr Val Gly Gly Gly Thr Val Pro Ala Gly Ser Gly Gly Gln Gly Gly Asn Ala Gly Gly Gly Gly Ala Gly Gly Gln Gly Gly Ala Asp 595 Gly Gly Ser Gly Gly Asp Gly Gly Asp Ala Gly Thr Gly Gly Asn Gly 615 Gly Asn Gly Gly Asn Arg Asn Ser Gly Asn Gly Thr Gly Gly Ala Gly Gly Asn Gly Gly Gly Ala Asn Gly Gly Ala Gly Gly Ala Gly Gly Ser Gly Gly Gly Thr Gly Gly Asn Gly Gly Ala Gly Gly Asp Ala Gly Asp Ala Gly Asn Gly Gly Asn Gly Asn Gly Thr Gly Asn Gly Gly Asn 675 Gly Gly Asn Gly Gly Ile Ala Gly Met Gly Gly Asn Gly Gly Ala Gly Thr Gly Ser Gly Asn Gly Gly Asn Gly Gly Ser Gly Gly Asn Gly Gly 705 710 Asn Ala Gly Met Gly Gly Asn Ser Gly Thr Gly Ser Gly Asp Gly Ala Gly Gly Asn Gly Gly Ala Ala Gly Thr Gly Gly Thr Gly Gly Asp 745

Gly Gly Leu Thr Gly Thr Gly Gly Thr Gly Gly Ser Gly Gly Thr Gly

760

- Gly Asp Gly Gly Asn Gly Gly Asn Gly Ala Asp Asn Thr Ala Asn Met 770 775 780
- Thr Ala Gln Ala Gly Gly Asp Gly Gly Asn Gly Gly Asp Gly Phe
  785 790 795 800
- Gly Gly Gly Ala Gly Ala Gly Gly Gly Leu Thr Ala Gly Ala Asn 805 810 815
- Gly Thr Gly Gly Gln Gly Gly Ala Gly Gly Asp Gly Gly Asn Gly Ala 820 825 830
- Ile Gly Gly His Gly Pro Leu Thr Asp Asp Pro Gly Gly Asn Gly Gly 835 840 845
- Thr Gly Gly Asn Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Ile Gly 850 855 860
- Ser Leu Gly Gly Gly Thr Gly Gly Asp Gly Gly Asn Gly Gly Asn Gly 865 870 875 880
- Gly Thr Gly Glu Gly Gly Glu Val Gly Gly Ala Gly Gly Thr Gly 885 890 895
- Gly Ala Ala Gly Asn Gly Gly Asp Gly Gly Thr Gly Gly Thr Gly Gly 900 905 910
- Gly Asp Gly Gly Ala Gly Gly Thr Gly Gly Thr Gly Gly 915 925
- Leu Gly Asp Pro Arg Val Gly Gly Ser Gly Gly Asp Gly Gly Thr Gly 930 935 940
- Gly Ser Gly Gly Ala Ala Gly Asn Gly Gly Asn Gly Gly Asn Ala Gly 945 950 955 960
- Ala Gly Gly Asn Gly Asn Gly Gly Thr Gly Gly Ala Gly Gly Ile Gly 965 970 975
- Gly Thr Gly Gly Asn Gly Gly Asp Ala Glu Pro Gly Val Pro Pro Gly 980 985 990
- Ala Gly Gly Ala Gly Gly Ala Gly Thr Thr Gly Gly Lys Gly Gly Thr 995 1000 1005
- Gly Gly Asn Gly Ser Gly Thr Gly Ser Gly Gly Thr Gly Gly Asp 1010 1015 1020
- Gly Gly Thr Gly Gly Gly Gly Asn Gly Gly Thr Gly Trp Asn 1025 1030 1035
- Gly Gly Lys Gly Asp Thr Gly Ser Gly Gly Gly Ala Gly Asp Gly 1040 1045 1050
- Gly Lys Ala Pro Ala Gly Gly Thr Gly Gly Ala Gly Gly Asp Gly

1055 1060 1065

Gly Ala Gly Gly Lys Gly Gly Ser Gly Gly Val 1070 1075

<210> 21

<211> 354

<212> PRT

<213> M. tuberculosis

<220>

<221> misc\_feature

<223> PPE

<220>

<221> misc feature

<223> gi | 1781260

<400> 21

Met Pro Gly Arg Phe Arg Asn Phe Gly Ser Gln Asn Leu Gly Ser Gly 1 5 10 15

Asn Ile Gly Ser Thr Asn Val Gly Ser Gly Asn Ile Gly Ser Thr Asn 20 25 30

Val Gly Ser Gly Asn Ile Gly Asp Thr Asn Phe Gly Asn Gly Asn Asn 35 40 45

Gly Asn Phe Asn Phe Gly Ser Gly Asn Thr Gly Ser Asn Asn Ile Gly 50 55 60

Phe Gly Asn Thr Gly Ser Gly Asn Phe Gly Phe Gly Asn Thr Gly Asn 65 70 75 80

Asn Asn Ile Gly Ile Gly Leu Thr Gly Asp Gly Gln Ile Gly Ile Gly 85 90 95

Gly Leu Asn Ser Gly Ser Gly Asn Ile Gly Phe Gly Asn Ser Gly Thr 100 105 110

Gly Asn Val Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Phe Gly
115 120 125

Asn Ser Gly Thr Ala Asn Thr Gly Phe Gly Asn Ala Gly Asn Val Asn 130 135 140

Thr Gly Phe Trp Asn Gly Gly Ser Thr Asn Thr Gly Leu Ala Asn Ala 145 150 155 160

Gly Ala Gly Asn Thr Gly Phe Phe Asp Ala Gly Asn Tyr Asn Phe Gly 165 170 175

```
Ser Leu Asn Ala Gly Asn Ile Asn Ser Ser Phe Gly Asn Ser Gly Asp
Gly Asn Ser Gly Phe Leu Asn Ala Gly Asp Val Asn Ser Gly Val Gly
                            200
Asn Ala Gly Asp Val Asn Thr Gly Leu Gly Asn Ser Gly Asn Ile Asn
Thr Gly Gly Phe Asn Pro Gly Thr Leu Asn Thr Gly Phe Phe Ser Ala
                    230
                                        235
Met Thr Gln Ala Gly Pro Asn Ser Gly Phe Phe Asn Ala Gly Thr Gly
                245
                                    250
Asn Ser Gly Phe Gly His Asn Asp Pro Ala Gly Ser Gly Asn Ser Gly
            260
                                265
Ile Gln Asn Ser Gly Phe Gly Asn Ser Gly Tyr Val Asn Thr Ser Thr
Thr Ser Met Phe Gly Gly Asn Ser Gly Val Leu Asn Thr Gly Tyr Gly
                        295
Asn Ser Gly Phe Tyr Asn Ala Ala Val Asn Asn Thr Gly Ile Phe Val
305
                    310
Thr Gly Val Met Ser Ser Gly Phe Phe Asn Phe Gly Thr Gly Asn Ser
Gly Leu Leu Val Ser Gly Asn Gly Leu Ser Gly Phe Phe Lys Asn Leu
                                345
                                                    350
Phe Gly
<210> 22
<211> 29
<212> PRT
<213> Pseudomonas aeruginosa
<220>
<221> misc feature
<223> KdpF protein
<220>
<221> misc feature
<223> gi 9947600
```

<400> 22

Met Thr Val Leu Asp Trp Leu Ser Leu Ala Leu Ala Thr Gly Leu Phe 1 5 10 15

Val Tyr Leu Leu Val Ala Leu Leu Arg Ala Asp Arg Ala <210> 23 <211> 352 <212> PRT <213> Pseudomonas aeruginosa <220> <221> misc feature <223> alginate regulatory protein AlgP <220> <221> misc\_feature <223> gi 9951563 <400> 23 Met Ser Ala Asn Lys Lys Pro Val Thr Thr Pro Leu His Leu Leu Gln Gln Leu Ser His Ser Leu Val Glu His Leu Glu Gly Ala Cys Lys Gln 20 Ala Leu Val Asp Ser Glu Lys Leu Leu Ala Lys Leu Glu Lys Gln Arg Gly Lys Ala Gln Glu Lys Leu His Lys Ala Arg Thr Lys Leu Gln Asp Ala Ala Lys Ala Gly Lys Thr Lys Ala Gln Ala Lys Ala Arg Glu Thr Ile Ser Asp Leu Glu Glu Ala Leu Asp Thr Leu Lys Ala Arg Gln Ala 90 Asp Thr Arg Thr Tyr Ile Val Gly Leu Lys Arg Asp Val Gln Glu Ser 100 Leu Lys Leu Ala Gln Gly Val Gly Lys Val Lys Glu Ala Ala Gly Lys 120 Ala Leu Glu Ser Arg Lys Ala Lys Pro Ala Thr Lys Pro Ala Ala Lys 135 Ala Ala Ala Lys Pro Ala Val Lys Thr Val Ala Ala Lys Pro Ala Ala 145

Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala 165 170 175

Lys Thr Ala Ala Ala Lys Pro Ala Ala Lys Pro Thr Ala Lys Pro Ala

180 185 190

Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Thr Ala Ala Ala Lys Pro 195 200 205

Ala Ala Lys Pro Ala Ala Lys Pro Val Ala Lys Pro Ala Ala Lys Pro 210 215 220

Ala Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys 225 230 235 240

Pro Val Ala Lys Pro Thr Ala Lys Pro Ala Ala Lys Thr Ala Ala Ala 245 250 255

Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala 260 265 270

Lys Pro Val Ala Lys Ser Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala 275 280 285

Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Val 290 295 300

Ala Ala Lys Pro Ala Ala Thr Lys Pro Ala Thr Ala Pro Ala Ala Lys 305 310 315 320

Pro Ala Ala Thr Pro Ser Ala Pro Ala Ala Ala Ser Ser Ala Ala Ser 325 330 335

Ala Thr Pro Ala Ala Gly Ser Asn Gly Ala Ala Pro Thr Ser Ala Ser 340 345 350

<210> 24

<211> 309

<212> PRT

<213> Pseudomonas aeruginosa

<220>

<221> misc feature

<223> polyhydroxyalkanoate synthesis protein PhaF

<220>

<221> misc feature

<223> gi 9951352

<400> 24

Met Ala Gly Lys Lys Ser Glu Lys Glu Ser Ser Trp Ile Gly Glu 1 5 10 15

Ile Glu Lys Tyr Ser Arg Gln Ile Trp Leu Ala Gly Leu Gly Ala Tyr 20 25 30

Ser Lys Val Ser Lys Asp Gly Ser Lys Leu Phe Glu Thr Leu Val Lys 35 40 45

Asp Gly Glu Lys Ala Glu Lys Glu Ala Lys Ser Asp Val Asp Ala Gln 50 55 60

Val Gly Ala Ala Lys Ala Ser Ala Arg Ser Ala Lys Ser Lys Val Asp
65 70 75 80

Glu Val Arg Asp Arg Ala Leu Gly Lys Trp Ser Glu Leu Glu Glu Ala 85 90 95

Phe Asp Lys Arg Leu Asn Ser Ala Ile Ser Arg Leu Gly Val Pro Ser 100 105 110

Arg Asn Glu Val Lys Glu Leu His Ser Lys Val Asp Thr Leu Thr Lys
115 120 125

Gln Ile Glu Lys Leu Thr Gly Val Ser Val Lys Pro Ala Ala Lys Ala 130 135 140

Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Ala Ala Lys
165 170 175

Pro Ala Ala Lys Pro Ala Ala Lys Lys Thr Ala Ala Lys Thr Ala Ala 180 185 190

Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro Thr Ala Lys Ala Ala 195 200 205

Ala Lys Pro Ala Thr Lys Pro Ala Ala Lys Ala Ala Lys Pro Ala 210 215 220

Ala Lys Pro Ala Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro 225 230 235 240

Ala Ala Ala Thr Ala Ala Lys Pro Ala Ala Lys Pro Ala Ala Lys Pro 245 250 255

Ala Ala Lys Lys Pro Ala Ala Lys Lys Pro Ala Ala Lys Pro Ala Ala
260 265 270

Ala Lys Pro Ala Ala Pro Ala Ala Ser Ser Ser Ala Pro Ala Ala Pro 275 280 285

Ala Ala Thr Pro Ala Ala Ser Ala Pro Ala Ala Asn Ala Pro Ala Thr 290 295 300

Pro Ser Ser Gln Gly

<210> 25

195

```
<211> 632
<212> PRT
<213> T. pallidum
<220>
<221> misc_feature
<223> dicarboxylate transporter (dctM)
<220>
<221> misc feature
<223> gi 3323280
<400> 25
Met Lys Gly Thr Arg Gly Gln Leu Val Leu Arg Ser Ile Ala Leu Leu
Leu Ile Gly Thr Leu Met Leu Leu Pro Leu Val Leu Phe Leu Ile Glu
Arg Ile Phe Gly Phe Leu Thr Arg Gly Val Gly Ser Glu Val Phe Ser
Ala His Glu Asp Phe Ile Phe Leu Phe Phe Ser Ser Asp Ala Ala
Val Ala Gln Leu Ala Phe Val Phe Ser Cys Val Ala Gly Ile Tyr Ala
Ala Arg Glu Arg Lys His Leu Ser Val Thr Leu Phe Ser Cys Asp Val
Asp Arg Pro Met His Arg Val Leu Ser Phe Leu Ser Ala Ile Cys Thr
                                105
Val Ala Val Leu Ser Ala Cys Phe Phe Ala Ser Gly Pro Asn Ile Val
        115
                            120
Ala Val Phe Arg Lys Glu Glu Ala Val Trp Gly Val Pro Leu Arg Trp
                        135
Ile Phe Thr Ala Leu Pro Cys Met Tyr Gly Ala Leu Leu Phe His Tyr
145
                    150
Ala Arg Glu Val Lys Cys Arg Thr Cys Val Ile Val Gly Leu Leu Val
                                    170
Gly Val Leu Ile Ser Thr Gly Ser Ile Ala Ser Val Leu Phe His Leu
                                185
Phe Asp Leu Thr Val Pro Leu Leu Asp Ser Val Phe His Gly Trp Val
```

200

205

Ala Val Gly Thr Arg Leu Phe Trp Pro Phe Val Leu Leu Leu Leu Leu Leu Ala Ala Gln Gly Leu Pro Leu Phe Ile Thr Leu Leu Ala Ile Ala Tyr Leu Ala Leu Ser Val Asp Gly Gly Tyr Val Asp Thr Leu Pro Leu Glu Gly Tyr Lys Ile Leu Thr Asp Thr Gly Gly Ile Val Ala Val Pro Leu Phe Ala Thr Ala Ser Leu Leu Leu Ala Arg Gly Ser Thr Gly Thr 280 Arg Leu Leu Arg Leu Val Lys Glu Ala Val Gly Trp Leu Arg Gly Gly 300 290 Ala Ala Val Ala Cys Val Ala Val Ala Ala Leu Phe Thr Ser Leu Thr Gly Val Ser Gly Val Thr Ile Leu Ala Leu Gly Ser Leu Phe Lys Leu 330 Ile Leu Thr Gly Asn Lys Tyr Pro Glu His Asp Ala Glu Ala Leu Ile 340 Thr Ser Ser Gly Ala Ile Gly Leu Leu Phe Pro Pro Ser Ala Ala Ile Ile Ile Phe Gly Ala Thr Asn Ile Leu Thr Val His Ile Val Asp Leu 370 Phe Lys Gly Ala Leu Leu Pro Gly Thr Leu Leu Val Leu Ser Ala Met Cys Leu Gly Val Ala Lys Asp Arg Thr Gln Val Arg Pro Ser Phe Ser 410 Trp Gln Leu Leu Val His Ala Val Arg Gly Ser Val Phe Asp Leu Ala 420 Leu Pro Val Cys Ile Ser Leu Gly Tyr Phe Ser Gly Thr Leu Asn Leu 440 Leu Gln Cys Ala Ser Leu Thr Thr Leu Leu Ala Phe Val Leu Gly Thr Trp Val Arg Arg Asp Phe Thr Val Lys Glu Ala Cys Ala Thr Ala Leu 465 Glu Ser Leu Pro Ile Val Gly Gly Ile Leu Ile Ile Val Ala Ala Ala 490

Lys Gly Leu Ser Phe Tyr Leu Val Asp Ala Asn Val Pro Asp Thr Leu

500 505 510

Ile Ala Phe Leu Gln His Ala Ile Ser Ser Lys Tyr Ala Phe Leu Leu 515 520 525

Leu Leu Asn Val Leu Leu Gly Val Gly Cys Ile Met Asp Leu Tyr 530 535 540

Ser Ala Ile Leu Val Ile Ser Pro Leu Val Leu Pro Leu Ala Val His 545 550 555 560

Phe Gly Val His Pro Val His Ala Ser Val Val Phe Leu Met Asn Leu 565 570 575

Glu Leu Gly Ala Leu Thr Pro Pro Ile Gly Met Asn Leu Phe Ile Ala 580 585 590

Ser Phe Ala Phe Glu Lys Pro Ile Val Tyr Leu Thr Arg Ala Ile Ala 595 600 605

Pro Phe Leu Leu Ala Gln Leu Gly Val Leu Leu Leu Thr Thr Tyr Ile 610 615 620

Pro Trp Leu Ser Thr Ala Phe Leu

<210> 26 <211> 653 <212> PRT

<213> Vibrio cholerae

<220>

<221> misc\_feature

<223> iron(III) ABC transporter, permease protein

<220>

<221> misc\_feature <223> gi|9654609

<400> 26

Met Ser Val Leu Arg Leu Thr Gly Leu Gly Ala Leu Thr Leu Leu Leu 1 5 10 15

Ala Leu Val Ser Leu Gln Trp Gly His Asn Leu Thr Leu Asn Glu Gln
20 25 30

Trp Gln Leu Val Leu Gly His Gln Ala Ala Gln Ser Phe Ala Gln Val 35 40 45

Asn Phe Ile Tyr Ala Gln Leu Pro Arg Ala Val Met Ala Ile Val Val 50 55 60

Gly Ala Val Leu Gly Leu Val Gly Ser Leu Met Gln Gln Leu Thr Gln Asn Arg Leu Thr Ser Pro Leu Thr Leu Gly Thr Ser Ser Gly Ala Trp Leu Gly Leu Ile Ile Val Asn Ile Trp Phe Ser Asp Trp Val Ala Asp 105 Tyr Ser Ala Leu Ala Ala Met Ala Gly Ala Leu Leu Ala Phe Ala Leu 120 Ile Ile Ser Ile Ala Gly Leu Arg Asn Leu Thr Gly Leu Pro Leu Val 135 Val Ser Gly Met Val Val Asn Ile Leu Leu Gly Ser Ile Ala Thr Ala 155 145 150 Leu Val Leu Leu Asn Glu Glu Phe Ala Gln Asn Val Phe Met Trp Gly 170 Ala Gly Asp Leu Ala Gln Asn Gly Trp Glu Trp Leu Thr Trp Leu Leu 185 Pro Arg Leu Ala Leu Val Phe Pro Leu Leu Phe Ala Pro Arg Val 200 195 Leu Thr Leu Leu Arq Leu Gly His Glu Gly Ala Ala Arg Gly Leu Ala Val Leu Pro Ala Phe Leu Phe Leu Met Ala Gly Gly Ile Trp Leu 230 235 240 Val Ser Ala Ser Ile Thr Ala Val Gly Val Ile Gly Phe Ile Gly Leu 250 Leu Thr Pro Asn Ile Ala Arg Ser Leu Gly Ala Arg Thr Thr Lys Met 265 Glu Leu Tyr Ser Ser Ala Leu Leu Gly Ala Leu Leu Leu Ala Thr 275 Asp Met Leu Ala Met Gly Leu Ser Val Trp Ala Glu Glu Val Val Pro Ser Gly Ile Thr Ala Ala Val Ile Gly Ala Pro Ala Leu Ile Trp Phe 315 310 Ser Arg Arg Gln Leu Gln Ala Gln Asp Ser Leu Ser Ile Ser Leu Ser 325 Ser His Arg Arg Ser Pro Ser Arg Trp Ala Val Met Leu Ile Ala Ala 345 Ala Leu Leu Leu Ala Leu Ser Leu His Ile Gly Trp Gln Met Glu Ser 355 360 365

Ala Ser Trp Ala Leu Pro Ser Glu Phe Gln Trp Pro Leu Arg Trp Pro 370 375 380

Arg Met Leu Thr Ala Leu Phe Ala Gly Val Gly Leu Ala Ile Ala Gly

390

Thr Leu Leu Gln Arg Leu Ile Tyr Asn Pro Leu Ala Ser Pro Asp Ile 405 410 415

Leu Gly Val Ser Ser Gly Ala Thr Phe Ala Leu Val Phe Ala Ser Leu
420 425 430

Phe Leu Gly Gln Ser Leu Gln Ser Thr His Trp Met Thr Ala Leu Leu 435 440 445

Gly Ser Ala Ala Val Leu Val Ala Leu Leu Leu Gly Arg Arg His 450 455 460

His Tyr Ala Pro Ser Ser Leu Ile Leu Thr Gly Ile Ala Ile Thr Ala 465 470 475 480

Leu Leu Glu Ala Leu Val Gln Phe Thr Leu Ala Lys Gly Thr Gly Asp 485 490 495

Ser Tyr Gln Ile Leu Leu Trp Leu Ser Gly Ser Thr Tyr Arg Ala Thr 500 505 510

Gly Glu Gln Ala Leu Leu Ser Val Gly Val Val Gly Leu Thr Leu 515 520 525

Leu Ala Leu Gly Leu Ser Arg Trp Leu Thr Leu Ile Ser Ile Gly Arg 530 535 540

Gly Phe Ala Ser Ala Arg Gly Leu Ser Ala Ser Arg Ala Ser Leu Val 545 550 555 560

Leu Leu Ile Leu Val Ala Leu Leu Cys Ala Leu Val Thr Ala Thr Met 565 570 575

Gly Pro Val Ser Phe Val Gly Leu Ile Ala Pro His Met Ala Met Met 580 585 590

Leu Gly Ala Gln Arg Ala Pro Ser Gln Leu Leu Leu Ala Ala Leu Val 595 600 605

Gly Gly Thr Leu Met Leu Trp Ala Asp Trp Leu Gly Gln Ala Leu Leu 610 620

Phe Pro Ala Gln Ile Ala Ala Gly Thr Leu Val Ala Ile Ile Gly Gly 625 630 635 640

Ser Tyr Phe Leu Leu Leu Leu Ser Gln Arg Ala Arg 645 650

<210> 27 <211> 356 <212> PRT <213> Vibrio cholerae <220> <221> misc feature <223> tolA protein <220> <221> misc\_feature <223> gi|9656364 <400> 27 Met Lys Glu Asn Lys Ser Arg Lys Ser Asn Asp Ala Lys Ser Ile Thr Ile Ser Leu Ala Met His Gly Ala Leu Val Ala Ile Leu Leu Trp Gly Ala Asp Phe Thr Met Ser Asp Pro Glu Pro Thr Gly Gln Met Ile Glu 35 Ala Val Val Ile Asp Pro Gln Leu Val Arg Gln Gln Ala Gln Gln Ile Arg Ser Gln Arg Glu Glu Ala Ala Lys Lys Glu Gln Glu Arg Leu Asp Lys Leu Arg Arg Glu Ser Glu Gln Leu Glu Lys Asn Arg Gln Ala Glu Glu Glu Arg Ile Arg Gln Leu Lys Glu Gln Gln Ala Lys Glu Ala Lys 105 Ala Ala Arg Glu Ala Glu Lys Leu Arg Glu Gln Lys Glu Gln Glu Arg 115 Leu Ala Ala Glu Gln Lys Ala Arg Glu Glu Lys Glu Arg Ala Ala Lys Ala Glu Ala Glu Arg Lys Val Lys Glu Glu Ala Ala Lys Lys Ala Glu Gln Glu Arg Val Ala Lys Glu Ala Ala Ala Ala Lys Ala Glu Gln Gln 165 Arg Ile Glu Arg Glu Lys Glu Ala Lys Leu Ala Glu Glu Lys Ala Lys

Arg Glu Lys Glu Val Ala Ala Lys Ala Glu Gln Glu Arg Leu Ala Lys

195 200 205

Glu Lys Ala Ala Lys Glu Ala Ala Asp Lys Ala Lys Lys Glu Lys Glu 210 215 220

Arg Ala Ala Lys Ala Glu Ala Glu Arg Lys Ala Gln Glu Ala Ala Leu 225 230 235 240

Asn Asp Ile Phe Gly Ser Leu Ser Glu Glu Ser Gln Gln Asn Asn Ala 245 250 255

Ala Arg Gln Gln Phe Val Thr Ser Glu Val Gly Arg Tyr Gly Ala Ile
260 265 270

Tyr Thr Gln Leu Ile Arg Gln Asn Leu Leu Val Glu Asp Ser Phe Arg 275 280 285

Gly Lys Gln Cys Arg Val Asn Leu Lys Leu Ile Pro Thr Gly Thr Gly 290 295 300

Ala Leu Leu Gly Ser Leu Thr Val Leu Asp Gly Asp Ser Arg Leu Cys 305 310 315 320

Ala Ala Thr Lys Arg Ala Val Ala Gln Val Asn Ser Phe Pro Leu Pro 325 330 335

Lys Asp Gln Pro Asp Val Val Glu Lys Leu Lys Asn Ile Asn Leu Thr 340 345 350

Val Ala Pro Glu 355

<210> 28

<211> 73

<212> PRT

<213> L. major

<220>

<221> misc\_feature

<223> hydrophilic surface protein 2

<220>

<221> misc feature

<223> gi | 1743289

<400> 28

Met Gly Ser Ser Cys Thr Lys Asp Ser Ala Lys Glu Pro Gln Lys Ser 1 5 10 15

Ala Gly Asn Ile Asp Thr Thr Thr Arg Ser Asp Glu Lys Asp Gly Val 20 25 30 <400> 29

Met Gly Ser Ser Cys Thr Lys Asp Ser Ala Lys Glu Pro Gln Lys Ser 1 5 10 15

Ala Asp Lys Ile Lys Ser Thr Asn Glu Thr Asn Gln Gly Gly Asn Ala 20 25 30

Ser Gly Ser Arg Lys Ser Ala Gly Gly Arg Ala Asn Glu Tyr Asp Pro 35 40 45

Lys Asp Asp Gly Phe Thr Pro Asn Asn Glu Asp Arg Cys Pro Lys Glu 50 60

Asp Gly His Ala Pro Lys Asn Asp Asp His Ala Pro Lys Glu Asp Gly 65 70 75 80

His Ala Pro Lys Asn Asp Asp His Ala Pro Lys Glu Asp Gly His Ala 85 90 95

Pro Lys Asn Asp Asp His Ala Pro Lys Glu Asp Gly His Ala Pro Lys
100 105 110

Asn Asp Asp His Ala Pro Lys Glu Asp Gly His Ala Pro Lys Asn Asp 115 120 125

Asp His Ala Pro Lys Glu Asp Gly His Ala Pro Lys Asn Asp Gly Asp 130 135 140

Val Gln Lys Lys Ser Glu Asp Gly Asp Asn Val Gly Glu Gly Lys 145 150 155 160

```
Gly Asn Glu Asp Gly Asn Asp Asp Gln Pro Lys Glu His Ala Ala Gly
                                   170
                165
Asn
<210> 30
<211> 106
<212> PRT
<213> Plasmodium falciparum
<220>
<221> misc feature
<223> predicted integral membrane protein
<220>
<221> misc_feature
<223> gi | 3845179
<400> 30
Met Tyr Ile Cys Phe Phe Phe Phe Phe Phe Leu Val Ile Lys Leu
Gly Glu Asp Glu Asn Phe Gly Ser Ser Cys Phe Tyr Ser Leu Gly Asn
Thr Lys Ile Leu Thr Thr Val Tyr Gly Pro Asn Pro Asp Ser Lys Tyr
                            40
Ala Thr Tyr Ser Lys Gly Lys Val Phe Leu Asp Val Lys Ser Leu Asn
Ile Asn Thr Ile Gly Ala Ser Asp Arg Val Leu Tyr Ile Tyr Gly Phe
Phe Phe Phe Phe Phe Phe Phe Phe Ile Leu Asn Arg Ser Tyr
                                    90
                85
Phe Phe Leu Val Leu Phe Ile Ile Phe Ile
                                105
            100
<210> 31
<211> 396
<212> PRT
<213> Plasmodium falciparum
<220>
<221> misc_feature
<223> Circumsporozoite (CS) protein
```

<220> <221> misc\_feature <223> gi|4493889

<400> 31

Met Arg Lys Leu Ala Ile Leu Ser Val Ser Ser Phe Leu Phe Val Glu

1 10 15

Ala Leu Phe Gln Glu Tyr Gln Cys Tyr Gly Ser Ser Ser Asn Thr Arg
20 25 30

Val Leu Asn Glu Leu Asn Tyr Asp Asn Ala Gly Thr Asn Leu Tyr Asn 35 40 45

Glu Leu Glu Met Asn Tyr Tyr Gly Lys Gln Glu Asn Trp Tyr Ser Leu 50 55 60

Lys Lys Asn Ser Arg Ser Leu Gly Glu Asn Asp Asp Gly Asn Asn Glu 65 70 75 80

Asp Asn Glu Lys Leu Arg Lys Pro Lys His Lys Lys Leu Lys Gln Pro 85 90 95

Ala Asp Gly Asn Pro Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn 100 105 110

Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Val Asp Pro Asn 115 120 125

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 130 135 140

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 145 150 155 160

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn
165 170 175

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 180 185 190

Ala Asn Pro Asn Val Asp Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 195 200 205

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 210 215 220

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 225 230 235 240

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 245 250 255

Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn Ala Asn Pro Asn 265 260 Lys Asn Asn Gln Gly Asn Gly Gln Gly His Asn Met Pro Asn Asp Pro 280 Asn Arg Asn Val Asp Glu Asn Ala Asn Ala Asn Ser Ala Val Lys Asn Asn Asn Asn Glu Glu Pro Ser Asp Lys His Ile Lys Glu Tyr Leu Asn 315 305 310 Lys Ile Gln Asn Ser Leu Ser Thr Glu Trp Ser Pro Cys Ser Val Thr 330 325 Cys Gly Asn Gly Ile Gln Val Arg Ile Lys Pro Gly Ser Ala Asn Lys 340 345 Pro Lys Asp Glu Leu Asp Tyr Ala Asn Asp Ile Glu Lys Lys Ile Cys 360 Lys Met Glu Lys Cys Ser Ser Val Phe Asn Val Val Asn Ser Ser Ile 375 Gly Leu Ile Met Val Leu Ser Phe Leu Phe Leu Asn 390 <210> 32 <211> 497 <212> PRT <213> B. burgdorferi <220> <221> misc feature <223> predicted coding region BB0553 <220> <221> misc\_feature <223> "Xaa" may be any amino acid <220> <221> misc feature <223> gi|2688482 <400> 32

<400> 34

Met Asn Lys Thr Lys Asn Arg Ser Leu Thr Tyr Phe Ile Ile Leu Ser 1 5 10 15

Cys Ile Ser Leu Phe Gly Ala Asn Asn Asn Thr Ile Ser Tyr Ser Ser 20 25 30

Ile Glu Ile Pro Leu Glu Asp Leu Ser Glu Glu Phe Lys Ser Ser Gly Asn Lys Ser Asp Gln Ile Asn Thr Ser Lys His Leu Asn Lys Asn Ile Val Ser Tyr Glu Asp Pro Lys Lys Gly Lys Asp Leu Lys Leu Pro Glu Asn Ile Arg Asp Lys Lys Leu Pro Gln Lys Arg Met Asp Glu Asn Asp 90 Leu Lys Ser Val Ile Glu Asn Tyr Glu Asn Lys Ile Lys Asn Ile Glu 105 Lys Leu Leu Lys Thr Lys Asn Gln Lys Thr Ser Glu Asn Glu Asn Lys 115 120 Lys Ile Glu Ser Ile Glu Lys Lys Ala Lys Lys Tyr Glu Ile Leu Thr Asn Lys Leu Lys Asn Glu Ile Val Glu Ile Lys Lys Leu Leu Asn Lys 150 Lys Ile Lys Pro Lys Glu Asp Glu Asn Tyr Glu Lys Ile Asn Ile Glu Asn Ile Glu Glu Glu Thr Asp Asp Phe Glu Asp Asn Tyr Glu Tyr Asn Asp Glu Ile Glu Xaa Thr Asn Glu Asp Asn Tyr Pro Ser Asn Glu 195 200 Gly Ile Ile Asn Asn Leu Lys Glu Asn Leu Asn Glu Asn Glu Lys Tyr 215 Tyr Ala Ile Asn Glu Lys Lys Ile Asp Glu Leu Glu Asp Arg Ile Asn 230 235 Glu Asn Glu Asn Thr Ile Leu Asp Leu Gln Arg Glu Leu Arg Asn Phe Lys Lys Lys Asp Asn Ser Asp Lys Asn Leu Glu Glu Ile Glu Glu Asn Leu Ser Ser Ile Gly Arg Ile Ile Asn Asp Leu Lys Arg Lys Ile Ser

Leu Ser Ser Ile Gly Arg Ile Ile Asn Asp Leu Lys Arg Lys Ile Ser
275

Ala Asn Glu Ala Ile Asn Lys Glu Asn Gln Lys Lys Ile Arg Thr Asp
290

Lys His Lys Leu Lys Glu Leu Glu Asp Lys Ile Lys Glu Asn Glu Glu
305

310

315

320

Thr Ile Leu Lys Leu Gln Lys Glu Leu Asn Asn Phe Lys Lys Glu

325 330 335

Ile Tyr Gln Lys Pro Leu Asn Glu Glu Thr Phe Thr Pro Ser Ile Thr 340 345 350

Ser Lys Asn Asp Asp Leu Glu Glu Asn Lys Lys Leu Lys Lys Glu Tyr 355 360 365

Leu Lys Pro Ile Glu Lys Lys Glu Ser Arg Asp Leu Glu Glu Asn Thr 370 375 380

Lys Ser Thr Pro Lys Thr Thr Met Ile Lys Thr Ala Asp Phe Gln Ile 385 390 395 400

Tyr Pro Asp Ile Tyr Leu Asn Asn Tyr Lys Phe Lys Glu Lys Gly Asp 405 410 415

Gln Phe Ala Phe Lys Lys Glu Asn Thr Tyr Tyr Ile Glu Ile Asp Pro 420 425 430

Thr Asn Asn Leu Asn Glu Ala Leu Lys Asn His Glu Ile Ile Ser Lys 435 440 445

Tyr Lys Phe Glu Lys Tyr Phe Ile Asn Pro Ile Leu Lys Asn Lys Glu 450 455 460

Glu Phe Phe Arg Asn Leu Ile Glu Val Lys Asn Ile His Glu Leu Gly 465 470 475 480

Ile Met Tyr Lys Asn Leu Lys Pro Glu Phe Lys Gln Ile Lys Ile Ile 485 490 495

Lys

<210> 33

<211> 31

<212> PRT

<213> B. burgdorferi

<220>

<221> misc feature

<223> predicted coding region BB0148

<220>

<221> misc\_feature

<223> gi 2688046

<400> 33

Met Pro Val Lys Lys Asn Ser Thr Lys Ile Lys Lys Lys Glu Thr Gln 1 5 10 15

```
Hardy (String 1991); string the general period of the country of the string of the str
```

```
Ile Ala Ile Ala Leu Lys Ile Ile Ile Ile Ile Tyr Phe Phe Asp
            20
<210> 34
<211> 30
<212> PRT
<213> B. burgdorferi
<220>
<221> misc feature
<223> predicted coding region BB0150
<220>
<221> misc_feature
<223> gi 2688045
<400> 34
Met Phe Gly Cys Leu Arg Ile His Val Phe Lys Ile Tyr Phe Ile Phe
Leu Ile Ile His Tyr Ile Leu Phe Ser Ile Leu Leu Met Ile
                               25
<210> 35
<211> 344
<212> PRT
<213> B. burgdorferi
<220>
<221> misc_feature
<223> predicted coding region BB0212
<220>
<221> misc_feature
<223> gi 2688103
<400> 35
Met Met Lys Lys Ile Lys Ser Glu Ile Asn Leu Lys Ile Glu Lys
                5
Asp Lys Asn Leu Ile Glu Leu Gly Lys Ile Leu Lys Asn Asn Asn Ile
Val Glu Leu Lys Asn Leu Asn His Tyr Pro Asn Leu Lys Leu Val Glu
Lys Glu Leu Tyr Gln Met Lys Ser Asn Leu Ser Lys Ser Glu Glu Asn
    50
                        55
                                            60
```

Glu Asn Ile Leu Lys Asn Leu Asn Lys Lys Ile Tyr Ile Leu Lys Lys 65 70 75 80

Glu Tyr Lys Ser Thr Ser Lys Ser Tyr Lys Lys Asn Leu Lys Glu Ile 85 90 95

Ala Lys Thr Ile Ile Glu Ile Tyr Pro Gln Asn Leu Glu Leu Ile Ser 100 105 110

Lys Tyr Asn Met Asn Phe Ser Lys Leu Lys Leu Glu Lys Tyr Lys Lys 115 120 125

Ile Glu Leu Ala Ser Asp His Lys Thr Lys Asn Tyr Leu Gln Arg Ile 130 135 140

Met Leu Glu Val Ser Ser Thr Ile Asn Asn Ile Ile Asn Met Ile Asn 145 150 155 160

Val Tyr Lys Ile Ser Lys Glu Phe Glu Lys Gln Val Phe Thr Lys Tyr 165 170 175

Tyr Pro Ser Glu Asn Phe Glu Ser Ile Met Asn Glu Phe Ser Leu Asn 180 185 190

Lys Lys Leu Asn Asn Val Ile Val Lys Glu Phe Lys Ile Ile Asn Glu
195 200 205

Ile Lys Thr Asn Ile Lys Asn Ile Lys Glu Glu Ile Lys Glu Ile Ile 210 215 220

Ser Thr Ser Lys Lys Glu Lys Ile Tyr Lys Lys Asn Thr Ile Lys Asn 225 230 235 240

Glu Ile Asn Val Ile Thr Lys Asn Lys Glu Asn Ile Leu Lys Lys Ile 245 250 255

Ala Glu Glu Phe Ile Glu Ile Thr Lys Lys Asp Lys Met Thr Ala Lys 260 265 270

Thr Asn Ala Ile Ser Ser Ile Ile Gln Lys Ile Glu Lys Ile Asn Gln 275 280 285

Lys Ile Leu Asn Leu Asn Asn Asp Leu Ile Lys Ile Thr Lys Gln Glu 290 295 300

Glu Ile Lys Asn Ile Gln Gln Lys Ile Gln Ala Leu Thr Lys Glu Lys 305 310 315 320

Asn Lys Ile Asn Asn Lys Leu Asp Ala Leu Thr Ser Lys Ile Glu Val 325 330 335

Ile Gln Asn Glu Leu Asp Asn Glu 340

<210> 36

```
<211> 30
    <212> PRT
    <213> B. burgdorferi
    <220>
    <221> misc feature
    <223> predicted coding region BB0425
    <220>
    <221> misc_feature
    <223> gi 2688333
    <400> 36
    Met Glu Asp Glu Arg Arg Glu Glu Leu Ser Lys Val Lys Ser Gln Lys
    Asn Lys Gln Asn Leu Leu Ile Phe Leu Asn Lys Lys Ile Lys
    <210> 37
    <211> 32
The that the total tall, and
    <212> PRT
    <213> B. burgdorferi
    <220>
    <221> misc_feature
    <223> predicted coding region BB0433
3
Mary Street
    <220>
    <221> misc feature
    <223> gi 2688343
<400> 37
    Met His Lys Phe Phe Lys Leu Ile Leu Lys Leu Phe Ser Phe Tyr Lys
                     5
    Glu Ile Leu Gly Phe Lys Arg Arg Ala Lys Phe Ile Phe Cys Tyr Leu
                                      25
                 20
    <210> 38
    <211> 38
    <212> PRT
    <213> B. burgdorferi
    <220>
     <221> misc_feature
    <223> predicted coding region BB0520
```

```
<221> misc_feature
                 <223> gi | 2688447
                 <400> 38
                Met Ser Lys Ser Thr Lys Asn Thr Thr Lys Ser Lys Asn Asp Thr Lys
                 Asn Ile Leu Ile Asn Lys Lys Ile Lys Phe Phe Ile Leu Thr Lys Lys
                 Tyr Thr Arg Thr Phe Tyr
                 <210> 39
                 <211> 36
                 <212> PRT
                 <213> B. burgdorferi
                 <220>
                 <221> misc feature
the time that the time is the time of time of the time of time of time of time of time of time of the time of time
                  <223> predicted coding region BB0609
                  <220>
                   <221> misc_feature
                  <223> gi 2688540
                  <400> 39
                 Met Thr Met Ile Ile Ile Ile Phe Tyr Lys Tyr Leu Ile Pro Lys Ser
Ile Lys Asp Lys Asn Asn Lys Ser His Lys Thr Phe Ile Lys Lys Phe
                   Ile Ile Lys Tyr
                                                    35
                   <210> 40
                   <211> 31
                   <212> PRT
                   <213> B. burgdorferi
                   <220>
                   <221> misc feature
                   <223> predicted coding region BB0822
```

<220>

<220>

<221> misc\_feature <223> gi|2688768

```
<400> 40
Met Pro Cys Gly Arg Lys Arg Lys Leu Lys Lys Ile Ser Thr His Lys
Arg Lys Lys Lys Arg Arg Lys Asn Arg His Lys Lys Lys Asn Lys
                                25
<210> 41
<211> 34
<212> PRT
<213> B. burgdorferi
<220>
<221> misc_feature
<223> predicted coding region BB0848
<220>
<221> misc_feature
<223> gi 2688793
<400> 41
Met Tyr Phe Cys Ile Ile Asp Leu Glu Phe Val Gly Val Leu Pro Tyr
Phe Phe Ile Tyr Lys Phe Gly Glu Phe Tyr Phe Ser Phe Phe Gly Lys
Trp Arg
<210> 42
<211> 51
<212> PRT
<213> C. jejuni
<220>
<221> misc_feature
<223> highly acidic protein
 <220>
 <221> misc feature
 <223> gi | 6967728
 <400> 42
Met Ala Tyr Glu Asp Glu Glu Asp Leu Asn Tyr Asp Asp Tyr Glu Asn
```

```
Glu Asp Glu Glu Tyr Pro Gln Asn His His Lys Asn Tyr Asn Tyr Asp
Asp Asp Asp Tyr Glu Tyr Asp Asp Asp Asn Asn Asp Asp Phe Tyr
                            40
Glu Met Asp
    50
<210> 43
<211> 41
<212> PRT
<213> C. jejuni
<220>
<221> misc feature
<223> hypothetical protein Cj0344
<220>
<221> misc_feature
<223> gi 6967819
<400> 43
Met Phe Gln Asn Ile Ile Lys Tyr Lys Asp Phe Ile Ile Phe Ile Leu
Asn Leu Lys Gln Asn Leu Tyr Leu Leu Ile Lys Ile Asn Leu Asp Phe
            20
Lys Asn Phe His Lys Ser Leu Asn Phe
        35
 <210> 44
 <211> 37
 <212> PRT
 <213> C. jejuni
 <220>
 <221> misc feature
 <223> hypothetical protein Cj0567
 <220>
 <221> misc_feature
 <223> gi | 6968034
 <400> 44
 Met Asp Lys Ile Gln Glu Asn Thr Lys Ile Glu Lys Ala Ile Leu Ala
                                     10
                 5
```

```
the stands of the same stand of the stand of
```

```
Glu Lys Gln Gln Ile Phe Leu Ile Gln Asn Lys Leu Ser Glu Ile Glu
                                25
Lys Asn Ile Lys Glu
       35
<210> 45
<211> 74
<212> PRT
<213> C. jejuni
<220>
<221> misc_feature
<223> small hydrophobic protein
<220>
<221> misc feature
<223> gi 6968265
<400> 45
Met Leu Glu Phe Ile Phe Thr Leu Ile Leu Asp Phe Thr Phe Tyr Ser
Ile Lys Thr Leu Glu Lys Val Phe Leu Gly Arg Thr Ala Leu Val Ile
            20
Leu Phe Val Val Phe Ile Ala Leu Phe Cys Val Lys Gly Leu Phe Leu
Tyr Ile Leu Leu Ala Leu Glu Leu Phe Leu Leu Tyr Leu Phe Leu
                        55
Gly Ile Leu Phe Leu Arg Phe Tyr Lys Ser
                    70
<210> 46
<211> 46
<212> PRT
<213> C. jejuni
<220>
 <221> misc_feature
 <223> very hypothetical protein Cj0974
 <220>
 <221> misc_feature
 <223> gi 6968409
 <400> 46
```

```
Met Leu Lys Met Ile Lys Ile Gln Lys Val Lys Ser Leu Leu Asp Leu
Val Lys Lys Leu Lys Asn Lys Gln Ser Leu Lys Ile Lys Asn Gln Thr
            20
Asn Thr Lys Glu Asn Leu Asn Lys Thr His Tyr Leu Thr Ile
                            40
<210> 47
<211> 78
<212> PRT
<213> C. jejuni
<220>
<221> misc_feature
<223> very hypothetical protein
<220>
<221> misc_feature
<223> gi|6968423
<400> 47
Met Leu Lys Ile Pro Tyr Phe Ser Phe Leu Lys Leu Asp Phe Glu Ile
Tyr His Leu Asn Thr Ser Lys Asn Phe Tyr Gly Phe Phe Ile Leu Tyr
            20
Phe Ser Phe Phe Ile Phe Lys Leu Ile Tyr Lys Phe Ser Lys Ser Asn
                             40
Lys Lys Ile Tyr Lys Lys Ile Ile Lys Leu Lys Lys Ile Ile Lys Asp
Asn Lys Tyr Leu Ile Phe Leu Cys Tyr Ile Leu Ile Asn Ile
 65
 <210> 48
 <211> 30
<212> PRT
 <213> C. jejuni
 <220>
 <221> misc_feature
 <223> hypothetical protein Cj0748
 <220>
 <221> misc_feature
 <223> gi 6968200
```

<400> 48

Met Leu Glu Thr Leu Lys Lys Tyr Ala Glu Asn Gln Gly Ile Glu Asp 1 5 10 15

Asn Tyr Pro Lys Lys Ile Tyr Asn Gln Lys Glu Lys Lys Pro 20 25 30

<210> 49

<211> 168

<212> PRT

<213> C. pneumoniae CWL029

<220>

<221> misc\_feature

<223> CT670 hypothetical protein

<220>

<221> misc feature

<223> gi 4377009

<400> 49

Met Ala Lys Tyr Pro Leu Glu Pro Val Leu Ala Ile Lys Lys Asp Arg
1 5 10 15

Val Asp Arg Ala Glu Lys Val Val Lys Glu Lys Arg Arg Leu Leu Glu 20 25 30

Ile Glu Gln Glu Lys Leu Arg Glu Lys Glu Ala Glu Arg Asp Lys Val

Lys Asn His Tyr Met Gln Lys Ile Gln Gln Leu Arg Asp Leu Leu Asp 50 55 60

Glu Gly Thr Thr Ser Asp Ala Val Leu Gln Ile Lys Ser Tyr Ile Lys 65 70 75 80

Val Val Ala Val Gln Leu Ser Glu Glu Glu Glu Lys Val Asn Lys Gln 85 90 95

Lys Glu Val Val Leu Ala Ala Ser Lys Glu Leu Glu Lys Ala Glu Val 100 105 110

Asn Leu Ala Lys Arg Arg Lys Glu Glu Glu Lys Thr Arg Leu His Lys 115 120 125

Glu Glu Trp Met Lys Glu Ala Leu Lys Glu Glu Ala Arg Ala Glu Glu

Lys Glu Gln Asp Glu Met Gly Gln Leu Leu Phe Gln Leu Arg Gln Lys

145 150 155 160

Lys Lys Arg Glu Ser Gly Gly Ser 165

<210> 50

<211> 444

<212> PRT

<213> C. pneumoniae CWL029

<220>

<221> misc feature

<223> CT579 hypothetical protein

<220>

<221> misc\_feature

<223> gi 4377120

<400> 50

Met Thr Ser Gly Val Ser Gly Ser Ser Ser Gln Asp Pro Thr Leu Ala 1 5 10 15

Ala Gln Leu Ala Gln Ser Ser Gln Lys Ala Gly Asn Ala Gln Ser Gly
20 25 30

His Asp Thr Lys Asn Val Thr Lys Gln Gly Ala Gln Ala Glu Val Ala 35 40 45

Ala Gly Gly Phe Glu Asp Leu Ile Gln Asp Ala Ser Ala Gln Ser Thr 50 55 60

Gly Lys Lys Glu Ala Thr Ser Ser Thr Thr Lys Ser Ser Lys Gly Glu 65 70 75 80

Lys Ser Glu Lys Ser Gly Lys Ser Lys Ser Ser Thr Ser Val Ala Ser 85 90 95

Ala Ser Glu Thr Ala Thr Ala Gln Ala Val Gln Gly Pro Lys Gly Leu 100 105 110

Arg Gln Asn Asn Tyr Asp Ser Pro Ser Leu Pro Thr Pro Glu Ala Gln
115 120 125

Thr Ile Asn Gly Ile Val Leu Lys Lys Gly Met Gly Thr Leu Ala Leu 130 135 140

Leu Gly Leu Val Met Thr Leu Met Ala Asn Ala Ala Gly Glu Ser Trp 145 150 155 160

Lys Ala Ser Phe Gln Ser Gln Asn Gln Ala Ile Arg Ser Gln Val Glu 165 170 175

- Ser Ala Pro Ala Ile Gly Glu Ala Ile Lys Arg Gln Ala Asn His Gln 180 185 190
- Ala Ser Ala Thr Glu Ala Gln Ala Lys Gln Ser Leu Ile Ser Gly Ile 195 200 205
- Val Asn Ile Val Gly Phe Thr Val Ser Val Gly Ala Gly Ile Phe Ser 210 215 220
- Ala Ala Lys Gly Ala Thr Ser Ala Leu Lys Ser Ala Ser Phe Ala Lys 225 230 235 240
- Glu Thr Gly Ala Ser Ala Ala Gly Gly Ala Ala Ser Lys Ala Leu Thr 245 250 255
- Ser Ala Ser Ser Ser Val Gln Gln Thr Met Ala Ser Thr Ala Lys Ala 260 265 270
- Ala Thr Thr Ala Ala Ser Ser Ala Gly Ser Ala Ala Thr Lys Ala Ala 275 280 285
- Ala Asn Leu Thr Asp Asp Met Ala Ala Ala Ala Ser Lys Met Ala Ser 290 295 300
- Asp Gly Ala Ser Lys Ala Ser Gly Gly Leu Phe Gly Glu Val Leu Asn 305 310 315 320
- Lys Pro Asn Trp Ser Glu Lys Val Ser Arg Gly Met Asn Val Val Lys 325 330 335
- Thr Gln Gly Ala Arg Val Ala Ser Phe Ala Gly Asn Ala Leu Ser Ser 340 345 350
- Ser Met Gln Met Ser Gln Leu Met His Gly Leu Thr Ala Ala Val Glu 355 360 365
- Gly Leu Ser Ala Gly Gln Thr Gly Ile Glu Val Ala His His Gln Arg
- Leu Ala Gly Gln Ala Glu Ala Gln Ala Glu Val Leu Lys Gln Met Ser 385 390 395 400
- Ser Val Tyr Gly Gln Gln Ala Gly Gln Ala Gly Gln Leu Gln Glu Gln 405 410 415
- Ala Met Gln Ser Phe Asn Thr Ala Leu Gln Thr Leu Gln Asn Ile Ala 420 425 430
- Asp Ser Gln Thr Gln Thr Thr Ser Ala Ile Phe Asn 435 440
- <210> 51
- <211> 493
- <212> PRT
- <213> C. pneumoniae CWL029

```
<220>
<221> misc_feature
      CT578 hypothetical protein
<223>
<220>
<221>
      misc feature
      gi 4377121
<223>
<400> 51
Met Ser Ile Ser Ser Ser Gly Pro Asp Asn Gln Lys Asn Ile Met
Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln Gln Asp Lys
Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg Gln Gly Lys
Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala Ser Gly Lys
Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro Gln Gln Gly
                    70
                                        75
Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala Gly Ala Asp
Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn Thr Ala Thr
Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys Ser Met Glu
                            120
Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln Met Lys Glu
                        135
    130
Val Glu Ala Val Val Ala Ala Leu Ser Gly Lys Ser Ser Gly Ser
                    150
Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val Thr Pro Arg
Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala Ile Gln Thr
Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala Ser Thr Gln
                            200
Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys Gln Ala Ile
                                            220
    210
                        215
```

Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys Ala Ala Glu 225 230 235 240

Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val Asn Thr Val 245 250 255

Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile Val Ala Ala 260 265 270

Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala Gly Ala Ala 275 280 285

Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala Ala Ala Thr 290 295 300

Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln Ala Val Lys 305 310 315 320

Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala Ala Ile Lys 325 330 335

Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr Leu Val Lys 340 345 350

Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val Phe Ala Lys 355 360 365

Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser Lys Val Ile 370 375 380

Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly Val Val Val 385 390 395 400

Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln Leu Ser Glu 405 410 415

Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly Lys Leu Gln 420 425 430

Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp Gln Gln Ala 435 440 445

Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu Met Thr Gln
450 455 460

Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr Ala Ala Ile 465 470 475 480

Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe 485 490

<210> 52

<211> 76

<212> PRT

<213> C. pneumoniae CWL029

```
<220>
<221> misc feature
<223> CT753 hypothetical protein
<220>
<221> misc feature
<223> gi 4377216
<400> 52
Met Arg Asn Met Glu Ala Lys Lys Ile Lys Glu Leu Ser Lys Glu Ala
Gln Leu Leu Lys Lys Leu Arg Glu Lys Ser Arg Val Leu Asp Glu Lys
Asn Lys Arg Lys Ala Trp Val Ala Lys Leu Val Ala Met Pro Glu Ser
Ile Arg Glu Ile Glu Lys Glu Glu Arg Val Glu Thr Pro Gln Leu Phe
    50
Gln Ala Ile Ala Glu Lys Ile Leu Glu Glu Gly Val
                    70
<210> 53
<211> 755
<212> PRT
<213> C. pneumoniae CWL029
<220>
<221> misc_feature
<223> CT456 hypothetical protein
<220>
<221> misc feature
<223> gi|4376866
<400> 53
Met Ala Ala Pro Ile Asn Gln Pro Ser Thr Thr Thr Gln Ile Thr Gln
Thr Gly Gln Thr Thr Thr Thr Thr Val Gly Ser Leu Gly Glu His
            20
Ser Val Thr Thr Gly Ser Gly Ala Ala Ala Gln Thr Ser Gln Thr
Val Thr Leu Ile Ala Asp His Glu Met Gln Glu Ile Ala Ser Gln Asp
```

60 55 50

Gly Ser Ala Val Ser Phe Ser Ala Glu His Ser Phe Ser Thr Leu Pro 75 70 Pro Glu Thr Gly Ser Val Gly Ala Thr Ala Gln Ser Ala Gln Ser Ala 90 Gly Leu Phe Ser Leu Ser Gly Arg Thr Gln Arg Arg Asp Ser Glu Ile 105 Ser Ser Ser Ser Asp Gly Ser Ser Ile Ser Arg Thr Ser Ser Asn Ala 115 120 Ser Ser Gly Glu Thr Ser Arg Ala Glu Ser Ser Pro Asp Leu Gly Asp 135 Leu Asp Ser Leu Ser Gly Ser Glu Arg Ala Glu Gly Ala Glu Gly Pro 150 155 Glu Gly Pro Gly Gly Leu Pro Glu Ser Thr Ile Pro His Tyr Asp Pro 170 165 Thr Asp Lys Ala Ser Ile Leu Asn Phe Leu Lys Asn Pro Ala Val Gln Gln Lys Met Gln Thr Lys Gly Gly His Phe Val Tyr Val Asp Glu Ala 200 195 Arg Ser Ser Phe Ile Phe Val Arg Asn Gly Asp Trp Ser Thr Ala Glu Ser Ile Lys Val Ser Asn Ala Lys Thr Lys Glu Asn Ile Thr Lys Pro 235 230 Ala Asp Leu Glu Met Cys Ile Ala Lys Phe Cys Val Gly Tyr Glu Thr 250 245 Ile His Ser Asp Trp Thr Gly Arg Val Lys Pro Thr Met Glu Glu Arg 265 Ser Gly Ala Thr Gly Asn Tyr Asn His Leu Met Leu Ser Met Lys Phe 280 275 Lys Thr Ala Val Val Tyr Gly Pro Trp Asn Ala Lys Glu Ser Ser Ser Gly Tyr Thr Pro Ser Ala Trp Arg Gly Ala Lys Val Glu Thr Gly 315 Pro Ile Trp Asp Asp Val Gly Gly Leu Lys Gly Ile Asn Trp Lys Thr 330 325

Thr Pro Ala Pro Asp Phe Ser Phe Ile Asn Glu Thr Pro Gly Gly Gly 345

340

- Ala His Ser Thr Ser His Thr Gly Pro Gly Thr Pro Val Gly Ala Thr
  355
  360
  365
- Val Val Pro Asn Val Asn Val Asn Leu Gly Gly Ile Lys Val Asp Leu 370 375 380
- Gly Gly Ile Asn Leu Gly Gly Ile Thr Thr Asn Val Thr Thr Glu Glu 385 390 395 400
- Gly Gly Gly Thr Asn Ile Thr Ser Thr Lys Ser Thr Ser Thr Asp Asp 405 410 415
- Lys Val Ser Ile Thr Ser Thr Gly Ser Gln Ser Thr Ile Glu Glu Asp 420 425 430
- Thr Ile Gln Phe Asp Asp Pro Gly Gln Gly Glu Asp Asp Asn Ala Ile 435 440 445
- Pro Gly Thr Asn Thr Pro Pro Pro Pro Gly Pro Pro Pro Asn Leu Ser 450 455 460
- Ser Ser Arg Leu Leu Thr Ile Ser Asn Ala Ser Leu Asn Gln Val Leu 465 470 475 480
- Gln Asn Val Arg Gln His Leu Asn Thr Ala Tyr Asp Ser Asn Gly Asn 485 490 495
- Ser Val Ser Asp Leu Asn Gln Asp Leu Gly Gln Val Val Lys Asn Ser 500 505 510
- Glu Asn Gly Val Asn Phe Pro Thr Val Ile Leu Pro Lys Thr Thr Gly 515 520 525
- Asp Thr Asp Pro Ser Gly Gln Ala Thr Gly Gly Val Thr Glu Gly Gly 530 535 540
- Gly His Ile Arg Asn Ile Ile Gln Arg Asn Thr Gln Ser Thr Gly Gln 545 550 555 560
- Ser Glu Gly Ala Thr Pro Thr Pro Gln Pro Thr Ile Ala Lys Ile Val 565 570 575
- Thr Ser Leu Arg Lys Ala Asn Val Ser Ser Ser Ser Val Leu Pro Gln 580 585 590
- Pro Gln Val Ala Thr Thr Ile Thr Pro Gln Ala Arg Thr Ala Ser Thr 595 600 605
- Ser Thr Thr Ser Ile Gly Thr Gly Thr Glu Ser Thr Ser Thr Thr Ser 610 615 620
- Thr Gly Thr Gly Thr Gly Ser Val Ser Thr Gln Ser Thr Gly Val Gly 625 630 635 640

Thr Pro Thr Thr Thr Arg Ser Thr Gly Thr Ser Ala Thr Thr Thr 645 650 Thr Ser Ser Ala Ser Thr Gln Thr Pro Gln Ala Pro Leu Pro Ser Gly 665 Thr Arg His Val Ala Thr Ile Ser Leu Val Arg Asn Ala Ala Gly Arg 680 Ser Ile Val Leu Gln Gln Gly Gly Arg Ser Gln Ser Phe Pro Ile Pro Pro Ser Gly Thr Gly Thr Gln Asn Met Gly Ala Gln Leu Trp Ala Ala 710 Ala Ser Gln Val Ala Ser Thr Leu Gly Gln Val Val Asn Gln Ala Ala 725 Thr Ala Gly Ser Gln Pro Ser Ser Arg Arg Ser Ser Pro Thr Ser Pro 745 Arg Arg Lys 755 <210> 54 <211> 221 <212> PRT <213> C. pneumoniae CWL029 <220> <221> misc\_feature <223> SET Domain protein

<220>

<221> misc feature

<223> gi|4377196

<400> 54

Met Ser Thr Val Thr Thr Glu Pro Cys Ser Ser Ile His Ile Ser Leu

Asn Asn Asp Trp Arg Asp Ser Gln Pro Tyr Ser Leu Asp Arg Ala Ser

Glu Leu Leu His Phe Arg Phe Leu Pro Ser Leu Val Phe Ser Asn Trp

Lys Val Glu Gln Gln Ile Glu Thr Leu Cys His Lys Ser Glu Lys Arg

Arg Leu Ile Ser Pro Leu Ala Lys Trp Leu Gly Lys Leu His Lys Gln 75

Asp Leu Cys Pro Pro Ala Pro Pro Val Ser Val Cys Trp Ile Asn 85 90 95

Ala His Val Gly Tyr Gly Val Phe Ala Arg Asp Glu Ile Ala Pro Trp 100 105 110

Thr Tyr Ile Gly Glu Tyr Thr Gly Ile Leu Arg His Arg Gln Ala Ile 115 120 125

Trp Met Asp Glu Asn Asp Tyr Cys Phe Arg Tyr Pro Met Pro Leu Phe 130 135 140

Thr Leu Arg Tyr Phe Thr Ile Asp Ser Gly Lys Gln Gly Asn Val Thr 145 150 155 160

Arg Phe Ile Asn His Ser Glu Gln Pro Asn Ala Glu Ala Ile Gly Val

Phe Ser Glu Gly Leu Phe His Val Ile Ile Arg Thr Val Ala Pro Ile 180 185 190

Tyr Ala Gly Gln Glu Ile Cys Tyr His Tyr Gly Pro Leu Tyr Trp Lys 195 200 205

His Arg Lys Lys Arg Glu Glu Phe Ile Pro Glu Glu Glu 210 215 220

<210> 55

<211> 98

<212> PRT

<213> C. pneumoniae CWL029

<220>

<221> misc\_feature

<223> hypothetical protein

<220>

<221> misc\_feature

<223> gi 4376483

<400> 55

Met Ser Tyr Pro Asp Ile Ser Asn Val Gln Ala Ser Ser Ile Gln Ser 1 5 10 15

Ala Leu Leu His Lys Thr Ser Asp Gln Ile Gln Gln Lys Arg Cys Phe 20 25 30

Lys Gln Ser Thr Phe Val Ile Leu Ala Val Ser Leu Val Ile Ile Gly

Ser Leu Phe Leu Leu Ala Gly Val Ala Ile Leu Thr Val Phe Ser His

```
50
```

the man that the the man

H HA KAN

55

, '

Gly Val Leu Ser Leu Val Phe Gly Val Leu Gly Ile Val Leu Gly Leu 70 65 Leu Leu Leu Ala Gly Gly Val Gly Leu Leu Val Glu Glu Ala Lys Ser 90 Leu Leu <210> 56 <211> 64 <212> PRT <213> C. pneumoniae CWL029 <220> <221> misc\_feature <223> CT382.1 hypothetical protein <220> <221> misc feature <223> gi 4376770 <400> 56 Met Ile Lys Gln Ala Cys Lys Phe Tyr Leu Leu Gln Cys Leu Leu Cys 5 Ala Leu Tyr Trp Leu Leu Lys Tyr Cys Arg Lys Leu Leu Lys Gly Thr 20 Leu His His Ser Glu Glu Thr Leu Tyr Gln Ala Leu Leu Ser Ser Leu Ile Asp Leu Leu Tyr Gln Leu Lys Gln Leu Pro Ala Pro Thr Asn Glu 55 50 <210> 57 <211> 50 <212> PRT <213> C. pneumoniae CWL029 <220> <221> misc\_feature

<223> hypothetical protein

<221> misc\_feature <223> gi|4376779

<220>

<400> 57 Met Arg Thr Tyr Thr Arg Ser Pro Lys Gln Ser Gly Val Glu Arg Lys 5 Gln Glu Asp Ala Glu Thr Ser Phe Ile Glu Thr Pro Lys Gly Ile Leu 25 Lys Lys Pro Gly Asn Lys Asp Pro Lys Gly Lys His Val His Trp Lys Asp Ser 50 <210> 58 <211> 775 <212> PRT <213> C. pneumoniae CWL029 <220> <221> misc feature <223> hypothetical protein <220> <221> misc\_feature <223> gi 4376756 <400> 58 Met Ala Ser Gly Ile Gly Gly Ser Ser Gly Leu Gly Lys Ile Pro Pro Lys Asp Asn Gly Asp Arg Ser Arg Ser Pro Ser Pro Lys Gly Glu Leu 25 Gly Ser His Glu Ile Ser Leu Pro Pro Gln Glu His Gly Glu Gly 40 35 Ala Ser Gly Ser Ser His Ile His Ser Ser Ser Phe Leu Pro Glu 70 75 65

Asp Gln Glu Ser Gln Ser Ser Ser Ala Ala Ser Ser Pro Gly Phe

Phe Ser Arg Val Arg Ser Gly Val Asp Arg Ala Leu Lys Ser Phe Gly

Asn Phe Phe Ser Ala Glu Ser Thr Ser Gln Ala Arg Glu Thr Arg Gln

Ala Phe Val Arg Leu Ser Lys Thr Ile Thr Ala Asp Glu Arg Arg Asp 125 120 115

Val Asp Ser Ser Ser Ala Ala Ala Thr Glu Ala Arg Val Ala Glu Asp 130 Ala Ser Val Ser Gly Glu Asn Pro Ser Gln Gly Val Pro Glu Thr Ser Ser Gly Pro Glu Pro Gln Arg Leu Phe Ser Leu Pro Ser Val Lys 170 Gln Ser Gly Leu Gly Arg Leu Val Gln Thr Val Arg Asp Arg Ile Val 185 Leu Pro Ser Gly Ala Pro Pro Thr Asp Ser Glu Pro Leu Ser Leu Tyr 200 Glu Leu Asn Leu Arg Leu Ser Ser Leu Arg Gln Glu Leu Ser Asp Ile 210 215 Gln Ser Asn Asp Gln Leu Thr Pro Glu Glu Lys Ala Glu Ala Thr Val Thr Ile Gln Gln Leu Ile Gln Ile Thr Glu Phe Gln Cys Gly Tyr Met 250 245 Glu Ala Thr Gln Ser Ser Val Ser Leu Ala Glu Ala Arg Phe Lys Gly 260 Val Glu Thr Ser Asp Glu Ile Asn Ser Leu Cys Ser Glu Leu Thr Asp Pro Glu Leu Gln Glu Leu Met Ser Asp Gly Asp Ser Leu Gln Asn Leu 300 Leu Asp Glu Thr Ala Asp Asp Leu Glu Ala Ala Leu Ser His Thr Arg 315 Leu Ser Phe Ser Leu Asp Asp Asn Pro Thr Pro Ile Asp Asn Asn Pro 330 Thr Leu Ile Ser Gln Glu Glu Pro Ile Tyr Glu Glu Ile Gly Gly Ala Ala Asp Pro Gln Arg Thr Arg Glu Asn Trp Ser Thr Arg Leu Trp Asn 360 Gln Ile Arg Glu Ala Leu Val Ser Leu Leu Gly Met Ile Leu Ser Ile 380 375 Leu Gly Ser Ile Leu His Arg Leu Arg Ile Ala Arg His Ala Ala Ala 390 385 Glu Ala Val Gly Arg Cys Cys Thr Cys Arg Gly Glu Glu Cys Thr Ser Ser Glu Glu Asp Ser Met Ser Val Gly Ser Pro Ser Glu Ile Asp Glu 420 425 430

Thr Glu Arg Thr Gly Ser Pro His Asp Val Pro Arg Arg Asn Gly Ser
435 440 445

Pro Arg Glu Asp Ser Pro Leu Met Asn Ala Leu Val Gly Trp Ala His
450 455 460

Lys His Gly Ala Lys Thr Lys Glu Ser Ser Glu Ser Ser Thr Pro Glu 465 470 475 480

Ile Ser Ile Ser Ala Pro Ile Val Arg Gly Trp Ser Gln Asp Ser Ser 485 490 495

Val Ser Phe Ile Val Met Glu Asp Asp His Ile Phe Tyr Asp Val Pro 500 505 510

Arg Arg Lys Asp Gly Ile Tyr Asp Val Pro Ser Ser Pro Arg Trp Ser 515 520 525

Pro Ala Arg Glu Leu Glu Glu Asp Val Phe Gly Asp Tyr Glu Val Pro 530 535 540

Ile Thr Ser Ala Glu Pro Ser Lys Asp Lys Asn Ile Tyr Met Thr Pro 545 550 555 560

Arg Leu Ala Thr Pro Ala Ile Tyr Asp Leu Pro Ser Arg Pro Gly Ser 565 570 575

Ser Gly Ser Ser Arg Ser Pro Ser Ser Asp Arg Val Arg Ser Ser Ser 580 585 590

Pro Asn Arg Arg Gly Val Pro Leu Pro Pro Val Pro Ser Pro Ala Met 595 600 605

Ser Glu Glu Gly Ser Ile Tyr Glu Asp Met Ser Gly Ala Ser Gly Ala 610 615 620

Gly Glu Ser Asp Tyr Glu Asp Met Ser Arg Ser Pro Ser Pro Arg Gly 625 630 635 640

Asp Leu Asp Glu Pro Ile Tyr Ala Asn Thr Pro Glu Asp Asn Pro Phe
645 650 655

Thr Gln Arg Asn Ile Asp Arg Ile Leu Gln Glu Arg Ser Gly Gly Ala
660 670

Ser Ala Ser Pro Val Glu Pro Ile Tyr Asp Glu Ile Pro Trp Ile His 675 680 685

Gly Arg Pro Pro Ala Thr Leu Pro Arg Pro Glu Asn Thr Leu Thr Asn 690 695 700

Val Ser Leu Arg Val Ser Pro Gly Phe Gly Pro Glu Val Arg Ala Ala 705 710 715 720

•

Leu Leu Ser Glu Ser Val Ser Ala Val Met Val Glu Ala Glu Ser Ile 725 730 735

Val Pro Pro Thr Glu Pro Gly Asp Gly Glu Ser Glu Tyr Leu Glu Pro
740 745 750

Leu Gly Gly Leu Val Ala Thr Thr Lys Ile Leu Leu Gln Lys Gly Trp
755 760 765

Pro Arg Gly Glu Ser Asn Ala 770 775

<210> 59

<211> 104

<212> PRT

<213> C. trachomatis

<220>

<221> misc\_feature

<223> hypothetical protein

<220>

<221> misc\_feature

<223> gi|3328515

<400> 59

Met Gly Asp Val Met Ile Gln Ser Val Lys Thr Glu Ser Gly Leu Val 1 5 10 15

Glu Gly His Arg Gly Ile Cys Asp Ser Leu Gly Arg Val Val Gly Ala 20 25 30

Leu Ala Lys Val Ala Lys Leu Val Val Ala Leu Ala Ala Leu Val Leu 35 40 45

Asn Gly Ala Leu Cys Val Leu Ser Leu Val Ala Leu Cys Val Gly Ala 50 55 60

Thr Pro Val Gly Pro Leu Ala Val Leu Val Ala Thr Thr Leu Ala Ser 70 75 80

Phe Leu Cys Ala Ala Cys Val Leu Phe Ile Ala Ala Lys Asp Arg Gly 85 90 95

Trp Ile Ala Ser Thr Asn Lys Cys
100

<210> 60

<211> 439

<212> PRT

<213> C. trachomatis

210

•

```
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi 3329021
<400> 60
Met Thr Thr Gly Val Arg Gly Asp Asn Ala Pro Asp Pro Ser Leu Leu
Ala Gln Leu Thr Gln Asn Ala Asn Ser Ala Ser Ala Ala Ser Thr Gly
Lys Asn Gly Gln Val Ala Gly Ala Lys Gln Glu Asn Val Asp Ala Ser
Phe Glu Asp Leu Gln Asp Ala Gln Gly Thr Gly Gly Ser Lys Lys
Ala Thr Ala Asn Gln Thr Ser Lys Ser Gly Lys Ser Glu Lys Ala Gln
                    70
Ala Ser Ser Gly Thr Ser Thr Thr Ser Val Ala Gln Ala Ser Gln
Thr Ala Thr Ala Gln Ala Val His Gly Ala Arg Asp Ser Gly Phe Asn
Ser Asp Gly Ser Ala Thr Leu Pro Ser Pro Thr Gly Thr Glu Val Asn
                            120
Gly Val Val Leu Arg Lys Gly Met Gly Thr Leu Ala Leu Met Gly Leu
    130
                        135
Ile Met Thr Leu Leu Ala Gln Ala Ser Ala Lys Ser Trp Ser Ser Ser
                    150
                                        155
Phe Gln Gln Asn Gln Ala Ile Gln Asn Gln Val Ala Met Ala Pro
                165
                                    170
Glu Ile Gly Asn Ala Ile Arg Thr Gln Ala Asn His Gln Ala Gln Ala
Thr Glu Leu Gln Ala Gln Gln Ser Leu Ile Ser Gly Ile Thr Asn Ile
                            200
```

Val Gly Phe Ala Val Ser Val Gly Gly Ile Leu Ser Ala Ser Lys

215

Ser Leu Gly Gly Leu Lys Ser Ala Ala Phe Thr Asn Glu Thr Ala Ser 240

Ala Thr Thr Ser Ala Thr Ser Ser Leu Ala Lys Thr Ala Thr Ser Ala 255

Leu Asp Asp Val Ala Gly Thr Ala Thr 265

Ser Gly Ala Ala Ser Ala Ala Ser Ala Ser Ser Ser Ala Ala Thr 265

Asp By Ala Ala Ser Ala Ala Ser Ala Ala Ser Ser Ala Ala Thr 265

Asp By Ala Ala Ala Ser Ala Ala Ser Ala Ala Ser Ser Ala Ala Thr Lys Leu Thr Gln

Asn Met Ala Glu Ser Ala Ser Lys Thr Leu Ser Gln Thr Ala Ser Lys 290 295 300

Ser Ala Gly Gly Leu Phe Gly Gln Ala Leu Asn Thr Pro Ser Trp Ser 305 310 315

Glu Lys Val Ser Arg Gly Met Asn Val Val Lys Thr Gln Gly Thr Arg 325 330 335

Ala Ala Lys Phe Ala Gly Arg Ala Leu Ser Ser Ala Met Asn Ile Ser 340 345 350

Gln Met Val His Gly Leu Thr Ala Gly Ile Asp Gly Ile Val Gly Gly 355 360 365

Val Ile Gly Ala Gln Val Ala Gln Glu Gln Arg Met Ala Gly Met Ala 370 375 380

Glu Ala Arg Ala Glu Glu Leu Lys Ser Leu Asn Ser Val Gln Ala Gln 385 390 395 400

Tyr Ala Ser Gln Ala Gln Gln Leu Gln Glu Gln Ser Gln Gln Ser Phe 405 410 415

Asn Ser Ala Leu Gln Thr Leu Gln Ser Ile Ser Asp Ser Ala Leu Gln 420 425 430

Thr Thr Ala Ser Met Phe Asn 435

<210> 61

<211> 168 <212> PRT

<213> C. trachomatis

<220>

<221> misc feature

<223> hypothetical protein

<220>

<221> misc\_feature <223> gi|3329121 <400> 61

Met Val Arg Tyr Pro Leu Glu Pro Val Leu Ser Ile Lys Lys Asp Arg 1 5 10 15

Val Asp Arg Ala Glu Lys Val Val Lys Glu Lys Arg Arg Leu Leu Glu 20 25 30

Leu Glu Gln Glu Lys Leu Arg Glu Arg Glu Ser Glu Arg Asp Lys Val 35 40 45

Lys Asn His Tyr Met Gln Lys Ile Arg Gln Leu Arg Glu Gln Leu Asp 50 55 60

Asp Gly Thr Thr Ser Asp Ala Ile Leu Lys Met Lys Ala Tyr Ile Lys 65 70 75 80

Val Val Ala Ile Gln Leu Ser Glu Glu Glu Glu Lys Val Asn Lys Gln 85 90 95

Lys Glu Asn Val Leu Ala Ala Ser Lys Glu Leu Glu Arg Ala Glu Val 100 105 110

Glu Leu Thr Lys Arg Arg Lys Glu Glu Glu Lys Thr Arg Leu His Lys
115 120 125

Glu Glu Trp Met Lys Glu Ala Leu Lys Glu Glu Ala Arg Gln Glu Glu
130 135 140

Lys Glu Gln Asp Glu Met Gly Gln Leu Leu His Gln Leu His Lys Gln 145 150 155 160

Lys Gln Arg Glu Ser Gly Glu Asn 165

<210> 62

<211> 819

<212> PRT

<213> H. influenzae

<220>

<221> misc feature

<223> conserved hypothetical protein

<220>

<221> misc\_feature

<223> gi | 1574537

<400> 62

Met Ala Asp Val Leu Ser Arg Phe Asn Ser Gly Lys Leu Trp Asp Phe

290

1				5				'	10	•				15	
Lys	Gly	Gly	Ile 20	His	Pro	Pro	Glu	Met 25	Lys	Ser	Gln	Ser	Asn 30	Ser	Gln
Pro	Leu	Arg 35	His	Leu	Pro	Leu	Gly 40	Thr	Asp	Phe	Tyr	Ile 45	Pro	Leu	Lys
Gln	His 50	Leu	Gly	Thr	Thr	Gly 55	Asn	Leu	Leu	Ile	Lys 60	Glu	Gly	Asp	Tyr
Val 65	Leu	Lys	Gly	Gln	Ala 70	Leu	Thr	Lys	Gly	Asp 75	Gly	Leu	Arg	Met	Leu 80
Pro	Val	His	Ala	Pro 85	Thr	Ser	Gly	Thr	Ile 90	Lys	Ser	Ile	Lys	Pro 95	Tyr
Val	Ala	Thr	His 100	Pro	Ser	Gly	Leu	Asp 105	Glu	Pro	Thr	Ile	His 110	Leu	Gln
Ala	Asp	Gly 115	Leu	Asp	Gln	Trp	Ile 120	Glu	Arg	Asn	Pro	Ile 125	Asp	Asp	Phe
Ser	Thr 130	Leu	Ser	Ser	Glu	Gln 135	Leu	Ile	His	Lys	Ile 140	Tyr	Gln	Ala	Gly
Ile 145	Ala	Gly	Leu	Gly	Gly 150	Ala	Val	Phe	Pro	Thr 155	Ala	Ala	Lys	Ile	Gln 160
Ser	Ala	Glu	Gln	Lys 165	Val	Lys	Leu	Leu	Ile 170	Ile	Asn	Gly	Ala	Glu 175	Cys
Glu	Pro	Tyr	Ile 180	Thr	Cys	Asp	Asp	Arg 185	Leu	Met	Arg	Glu	Arg 190	Ala	Asp
Glu	Ile	Ile 195	Lys	Gly	Ile	Arg	Ile 200	Leu	Arg	Tyr	Ile	Leu 205	His	Pro	Glu
Lys	Val 210	Val	Ile	Ala	Ile	Glu 215	Asp	Asn	Lys	Pro	Glu 220	Ala	Ile	Ser	Ala
Ile 225	Arg	Asn	Ala	Leu	Gln 230	Gly	Ala	Asn	Asp	Ile 235	Ser	Ile	Arg	Val	Ile 240
Pro	Thr	Lys	Tyr	Pro 245	Ser	Gly	Ala	Thr	Lys 250		Leu	Ile	Tyr	Leu 255	Leu
Thr	Gly	Ile	Glu 260		Pro	Ser	Gly	Glu 265		Ser	Ser	Ser	Ile 270	Gly	Val
Leu	Met	Gln 275		Val	Gly	Thr	Met 280		Ala	Ile	Lys	Arg 285		Ile	Ile

81/155

300

Asn Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asn Lys

295

Ile Ala Glu Lys Gly Asn Tyr Trp Val Arg Leu Gly Thr Pro Ile Ser 310 305 Gln Ile Leu Ser Asp Ala Gly Tyr Gln Phe Asp Lys His Phe Pro Ile 330 Phe Ala Gly Gly Pro Met Met Gly Leu Glu Leu Pro Asn Leu Asn Ala 345 340 Pro Val Thr Lys Leu Val Asn Cys Leu Leu Ala Pro Asp Tyr Leu Glu Tyr Ala Glu Pro Glu Ala Glu Gln Ala Cys Ile Arg Cys Ser Ser Cys 370 Ser Asp Ala Cys Pro Val Asn Leu Met Pro Gln Gln Leu Tyr Trp Phe 390 395 Ala Arg Ser Glu Asp His Lys Lys Ser Glu Glu Tyr Ala Leu Lys Asp 410 Cys Ile Glu Cys Gly Ile Cys Ala Tyr Val Cys Pro Ser His Ile Pro 420 Leu Ile Gln Tyr Phe Arg Gln Glu Lys Ala Lys Ile Trp Gln Ile Lys 440 Glu Lys Gln Lys Lys Ser Asp Glu Ala Lys Ile Arg Phe Glu Ala Lys 450 Gln Ala Arg Met Glu Arg Glu Glu Glu Arg Lys Ala Arg Ser Gln 470 Arg Ala Ala Gln Ala Arg Arg Glu Glu Leu Ala Gln Thr Lys Gly Glu 490 Asp Pro Val Lys Ala Ala Leu Glu Arg Leu Lys Ala Lys Lys Ala Asn 505 Glu Thr Glu Ser Thr Gln Ile Lys Thr Leu Thr Ser Glu Lys Gly Glu 520 Val Leu Pro Asp Asn Thr Asp Leu Met Ala Gln Arg Lys Ala Arg Arg 540 530 535 Leu Ala Arg Gln Gln Ala Ala Ser Gln Val Glu Asn Gln Gln Gln 550 Thr Gln Pro Thr Asn Ala Lys Lys Ala Ala Val Ala Ala Ala Leu Ala 570 Arg Ala Lys Ala Lys Leu Ala Gln Ala Asn Ser Thr Ser Glu Ala

590

585

580

Ile Ser Asn Ser Gln Thr Ala Glu Asn Gln Val Glu Lys Thr Lys Ser

Ala Val Glu Lys Thr Gln Glu Asn Ser Thr Ala Leu Asp Pro Lys Lys 610 615 620

Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys Lys Leu Ala 625 630 635 640

Gln Thr Asn Ser Thr Ser Glu Ala Ile Ser Asn Ser Gln Thr Ala Glu 645 650 655

Asn Glu Val Glu Lys Thr Lys Ser Ala Val Glu Lys Thr Glu Glu Asn 660 665 670

Ser Thr Ala Leu Asp Ala Lys Lys Ala Ala Ile Ala Ala Ile Ala 675 680 685

Arg Ala Lys Ala Lys Lys Leu Ala Gln Ala Asn Ser Ala Ser Glu Ala 690 695 700

Ile Ser Asn Ser Gln Thr Ala Glu Asn Glu Val Glu Lys Thr Lys Ser 705 710 715 720

Ala Val Glu Lys Thr Gln Gln Asn Ser Thr Ala Leu Asp Pro Lys Lys 725 730 735

Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys Leu Ala
740 745 750

Gln Ala Asn Ser Thr Ser Glu Ala Ile Ser Asn Ser Gln Thr Ala Glu
755 760 765

Asn Glu Val Glu Lys Thr Lys Ser Ala Val Glu Lys Thr Gln Glu Asn 770 775 780

Ser Thr Ala Leu Asp Pro Lys Lys Ala Ala Val Ala Ala Ala Ile Ala 785 790 795 800

Arg Ala Lys Ala Lys Leu Ala Lys Thr Gln Ala Thr Leu Glu Asn 805 810 815

Asn Gln Glu

<210> 63

<211> 52

<212> PRT

<213> H. influenzae

<220>

<221> misc\_feature

<223> predicted coding region HI1562

```
<220>
<221> misc_feature
<223> gi | 1574414
<400> 63
Met Leu Ser Lys Asp Pro Lys Val Leu Ile Lys Leu Gly Glu Leu Glu
Lys Asp Lys Ser Lys Ala Lys Lys Tyr Phe Gly Asp Ala Cys Asp Leu
Arg Ser Gln Glu Gly Cys Asp Lys Tyr Arg Glu Leu Asn Gln Lys Gln
Asp Thr Asn Lys
    50
<210> 64
<211> 150
<212> PRT
<213> H. influenzae
<220>
<221> misc_feature
<223> conserved hypothetical protein
<220>
<221> misc_feature
<223> gi | 1574625
<400> 64
Met Thr Leu Gln Leu Asn Thr Ile Ala Leu Leu Leu Val Ile Leu Leu
Ile Leu Gly Val Leu Ser Asn Asn Ser Thr Ile Thr Ile Ser Ala Ala
            20
Val Leu Leu Ile Met Gln Gln Thr Phe Leu Ser Ser His Ile Pro Leu
                             40
Leu Glu Lys Tyr Gly Val Lys Ile Gly Ile Ile Ile Leu Thr Ile Gly
Val Leu Ser Pro Leu Val Ser Gly Lys Ile Gln Leu Pro Asp Leu Ser
Gly Phe Leu Ser Trp Lys Met Ala Leu Ser Ile Ser Val Gly Val Leu
                                     90
Val Ala Trp Leu Ala Gly Lys Gly Val Pro Leu Met Gly Glu Gln Pro
```

```
100 105 110
```

Ile Leu Val Thr Gly Leu Leu Ile Gly Thr Ile Ile Gly Val Ala Phe
115 120 125

Leu Gly Gly Ile Pro Val Gly Pro Leu Ile Ala Ala Gly Ile Leu Ala 130 135 140

Leu Leu Gly Lys Ile 145 150

<210> 65

<211> 129 <212> PRT

<213> H. influenzae

<220>

<221> misc\_feature

<223> predicted coding region HI1339

<220>

The same than the trail that will

The first the

THE THE THE

<221> misc\_feature

<223> gi|1574799

<400> 65

Met Glu Lys Ile Met Lys Lys Leu Thr Leu Ala Leu Val Leu Gly Ser 1 5 10 15

Ala Leu Val Val Thr Gly Cys Phe Asp Lys Gln Glu Ala Lys Gln Lys
20 25 30

Val Glu Asp Thr Lys Gln Thr Val Ala Ser Val Ala Ser Glu Thr Lys 35 40 45

Asp Ala Ala Asn Thr Met Thr Glu Val Lys Glu Lys Ala Gln Gln 50 55 60

Leu Ser Thr Asp Val Lys Asn Lys Val Ala Glu Lys Val Glu Asp Ala 65 70 75 80

Lys Glu Val Ile Lys Ser Ala Thr Glu Ala Ala Ser Glu Lys Val Gly 85 90 95

Glu Met Lys Glu Ala Ala Ser Glu Lys Ala Ser Glu Met Lys Glu Ala 100 105 110

Val Ser Glu Lys Ala Thr Gln Ala Val Asp Ala Val Lys Glu Ala Thr 115 120 125

Lys

```
<210> 66
<211> 136
<212> PRT
<213> H. influenzae
<220>
<221> misc feature
<223> predicted coding region HI1462.1
<220>
<221> misc_feature
<223> "Xaa" may be any amino acid
<220>
<221> misc_feature
<223> gi 3212225
<400> 66
Met Xaa Gln Ser Asn Tyr Ser Met Glu Lys Ile Met Lys Lys Leu Thr
Leu Ala Leu Val Leu Gly Ser Ala Leu Val Val Thr Gly Cys Phe Asp
Lys Gln Glu Ala Lys Gln Lys Val Glu Asp Thr Lys Gln Thr Val Ala
Ser Val Ala Ser Glu Thr Lys Asp Ala Ala Ala Asn Thr Met Thr Glu
Val Lys Glu Lys Ala Gln Gln Leu Ser Thr Asp Val Lys Asn Lys Val
Ala Glu Lys Val Glu Asp Ala Lys Glu Val Ile Lys Ser Ala Thr Glu
Ala Ala Ser Glu Lys Val Gly Glu Met Lys Glu Ala Ala Ser Glu Lys
Ala Ser Glu Met Lys Glu Ala Val Ser Glu Lys Ala Thr Gln Ala Val
                            120
Asp Ala Val Lys Glu Ala Thr Lys
    130
                        135
<210> 67
<211> 113
<212> PRT
<213> H. influenzae
<220>
```

```
<221> misc feature
<223> conserved hypothetical protein
<220>
<221> misc_feature
<223> gi | 1574607
<400> 67
Met Phe Thr Asp Trp Lys Glu His Thr Ser His Val Lys Lys Ser Phe
Gly Glu Leu Gly Lys Gln Tyr Pro Lys Met Leu Gln Ala Tyr Gln Ala
Leu Gly Ala Ala Ala Glu Gly Asn Val Leu Asp Ala Lys Thr Arg
Glu Leu Ile Ala Leu Ala Val Ala Val Thr Thr Arg Cys Glu Ser Cys
Ile Ser Ala His Ala Glu Glu Ala Val Lys Ala Gly Ala Ser Glu Ala
                    70
Glu Val Ala Ala Ala Leu Ala Thr Ala Ile Ala Leu Asn Ala Gly Ala
Ala Tyr Thr Tyr Ser Leu Arg Ala Leu Glu Ala Tyr Ser Val Gln Lys
            100
                                105
Ala
<210> 68
<211> 33
<212> PRT
<213> H. pylori
<220>
<221> misc feature
<223> predicted coding region HP0131
<220>
<221> misc_feature
<223> gi 2313229
<400> 68
Met Pro Tyr Pro Phe Met Ser Phe Lys Gln Thr Phe Tyr Tyr Lys Met
                5
```

```
Phe
<210> 69
<211> 12
<212> PRT
<213> H. pylori
<220>
<221> misc_feature
<223> predicted coding region HP0429
<220>
<221> misc_feature
<223> gi|2313552
<400> 69
Met Asn Glu Asn Gly Lys Lys Glu Ala Leu Gln Leu
<210> 70
<211> 26
<212> PRT
<213> H. pylori
<220>
<221> misc_feature
<223> predicted coding region HP0560
<220>
<221> misc_feature
<223> gi|2313684
<400> 70
Met Gly Ile Ile Tyr Leu Ile Leu Phe Leu Ile Val Ile Tyr Leu Leu
                5
                                                       15
Tyr Arg Ile Leu Asp Val Leu Glu Gln Lys
            20
<210> 71
<211> 48
<212> PRT
<213> H. pylori
<220>
```

The state that the state of the state of

Glu Ser Lys Thr Met Lys Glu Arg Phe Lys Thr Leu Phe Phe Lys Ile

<400> 73

```
<221> misc_feature
<223> predicted coding region HP0756
<220>
<221> misc_feature
<223> gi 2313894
<400> 71
Met Lys Asp Tyr Glu Asp Glu Leu Glu Asp Phe Glu Glu Glu Glu Leu
Glu Gly Phe Glu Glu Glu Asp Glu Glu Tyr Gly Asp Tyr Lys Asn Val
Tyr Asp Asp Asp Tyr Glu Asp Tyr Asn Ser Asp Tyr Glu Glu Glu
<210> 72
<211> 23
<212> PRT
<213> H. pylori
<220>
<221> misc feature
<223> predicted coding region HP1500
<220>
<221> misc_feature
<223> gi 2314686
<400> 72
Met Cys Ser Asn Ser Ser Ser Leu Lys Ile Tyr Ser Leu Glu Ser Asn
                                   10
Phe Ser Phe Asn Ser Leu Phe
            20
<210> 73
<211> 1805
<212> PRT
<213> M. genitalium
<220>
<221> misc feature
<223> gi|1045905
```

- Met Lys Pro Phe Asp Lys Lys Pro Ser Leu Gln Pro Ile Tyr Asp Ile 1 5 10 15
- Gly Phe Asp Asp Gly Tyr Leu Gln Ser Glu Tyr Glu Lys Asn Arg Ser 20 25 30
- Lys Thr Asp Val Asp Lys Ile Glu Asn Gln Leu Leu Lys Glu Ile Lys 35 40 45
- Ser Leu Glu Asp Glu Leu Lys Asn Leu Lys Gly Leu Lys Asn Gln Ala 50 55 60
- Glu Asp Asn Pro Glu Leu Asp Lys Lys Ile Asn His Leu Glu Val Asp 65 70 75 80
- Leu Asn Arg Leu Val Asn Glu Tyr Lys Asn Phe Gln Phe Gln Lys Asn 85 90 95
- His Met Val Asp Lys Val Ser Glu Leu Asp Asn Leu Thr Arg Phe Tyr
  100 105 110
- Lys Asn Glu Leu Thr Arg Leu Gln Gln Glu Asn Ala Asp Phe Leu Asn 115 120 125
- Ser Lys Tyr Ala Asn Leu Ala Asn Phe Gln Ala Asn Tyr His Asn Lys 130 135 140
- Leu Asn Asp Phe His Arg Leu Ile Glu Asn Gln Asn Gln Thr Ile Asn 145 150 155 160
- Arg Leu Asn Gln Lys Ile Asn Gly Asn Gln Asn Leu Ile Asp Asn Asn 165 170 175
- Val Ala Leu Leu Gln Asn Pro Asn Ile Thr Val Glu Lys Lys Asn Tyr 180 185 190
- Leu Leu Asn Val Ile Asp Gln Leu Tyr Asn Glu Leu Asp Gln Leu Glu
  195 200 205
- Asn Gln Lys Arg Leu Leu Ser Ile Glu Tyr Glu Asn Thr Tyr Arg Glu 210 215 220
- Leu Val Ser Ala Asp Asn Glu Leu Gln Asn Val Tyr Glu Asn Ile Asp 225 230 235 240
- Gln Asn Gln Ile Gln Phe Lys His Gln Tyr Gln Thr Tyr Arg Asp Glu 245 250 255
- Leu Ser Gln Leu Glu Arg Lys Ile Gln Leu Thr Lys Gln Glu Leu Val 260 265 270
- Asp Lys Glu Ser Ala Leu Arg Val Lys Ile Asp Asp Ala Asp Phe Tyr
- Ile Asn Ala Arg Leu Ala Glu Leu Asp Asp Val Ala Lys Gln Leu Ser

295 290 Phe Gln Asp Gly Ile Thr Lys Gln Asn Ala Gln His Val Glu Asp Lys 310 305 Leu Val Ala Leu Asn Lys Glu Lys Asp Arg Leu Asn Thr Gln Lys Glu Ala Phe Phe Asn Leu Arg Gln Ser Ala Leu Ile Asp Ile Asn Lys Leu 345 Gln Glu Asn Glu Leu Phe Ala Lys His Leu Glu His Gln Gln Asn 355 360 Glu Phe Glu Gln Lys Gln Ser Asp Ser Leu Leu Lys Leu Glu Thr Glu Tyr Lys Ala Leu Gln His Lys Ile Asn Glu Phe Lys Asn Glu Ser Ala 385 390 395 Thr Lys Ser Glu Glu Leu Leu Asn Gln Glu Arg Glu Leu Phe Glu Lys 405 410 Arg Arg Glu Ile Asp Thr Leu Leu Thr Gln Ala Ser Leu Glu Tyr Glu 425 His Gln Arg Glu Ser Ser Gln Leu Leu Lys Asp Lys Gln Asn Glu Val 435 Lys Gln His Phe Gln Asn Leu Glu Tyr Ala Lys Lys Glu Leu Asp Lys Glu Arg Asn Leu Leu Asp Gln Gln Lys Lys Val Asp Ser Glu Ala Ile 470 Phe Gln Leu Lys Glu Lys Val Ala Gln Glu Arg Lys Glu Leu Glu Glu Leu Tyr Leu Val Lys Lys Gln Lys Gln Asp Gln Lys Glu Asn Glu Leu 505 Leu Phe Phe Glu Lys Gln Leu Lys Gln His Gln Ala Asp Phe Glu Asn 515 520

Leu Phe Phe Glu Lys Gln Leu Lys Gln His Gln Ala Asp Phe Glu Asn Glu Leu Glu Ala Leu Glu Ala Lys Gln Gln Gln Gln Gln Gln Gln Gln Gln Asp Sab Ala Lys His Ala Leu Glu Arg Ser Phe Ile Lys Leu Glu Asp Lys Glu Lys Asp Leu Asn Thr 545

Lys Ala Gln Gln Ile Ala Asn Glu Phe Ser Gln Leu Lys Thr Asp Lys 575

Ser Lys Ser Ala Asp Phe Glu Leu Met Leu Gln Asn Glu Tyr Glu Asn 580 585 590

Leu Gln Gln Glu Lys Gln Lys Leu Phe Gln Glu Arg Thr Tyr Phe Glu
595 600 605

Arg Asn Ala Ala Val Leu Ser Asn Arg Leu Gln Gln Lys Arg Glu Glu 610 615 620

Leu Leu Gln Gln Lys Glu Thr Leu Asp Gln Leu Thr Lys Ser Phe Glu 625 630 635 640

Gln Glu Arg Leu Ile Asn Gln Arg Glu His Lys Glu Leu Val Ala Ser 645 650 655

Val Glu Lys Gln Lys Glu Ile Leu Gly Lys Lys Leu Gln Asp Phe Ser 660 665 670

Gln Thr Ser Leu Asn Ala Ser Lys Asn Leu Ala Glu Arg Glu Met Ala 675 680 685

Ile Lys Phe Lys Glu Lys Glu Ile Glu Ala Thr Glu Lys Gln Leu Leu 690 695 700

Asn Asp Val Asn Asn Ala Glu Val Ile Gln Ala Asp Leu Ala Gln Leu 705 710 715 720

Asn Gln Ser Leu Asn Gln Glu Arg Ser Glu Leu Gln Asn Ala Lys Gln
725 730 735

Arg Ile Ala Asp Phe His Asn Asp Ser Leu Lys Lys Leu Asn Glu Tyr
740 745 750

Glu Leu Ser Leu Gln Lys Arg Leu Gln Glu Leu Gln Thr Leu Glu Ala 755 760 765

Asn Gln Lys Gln His Ser Tyr Gln Asn Gln Ala Tyr Phe Glu Gly Glu 770 775 780

Leu Asp Lys Leu Asn Arg Glu Lys Gln Ala Phe Leu Asn Leu Arg Lys
785 790 795 800

Lys Gln Thr Met Glu Val Asp Ala Ile Lys Gln Arg Leu Ser Asp Lys 805 810 815

His Gln Ala Leu Asn Met Gln Gln Ala Glu Leu Asp Arg Lys Thr His 820 825 830

Glu Leu Asn Asn Ala Phe Leu Asn His Asp Ala Asp Gln Lys Ser Leu 835 840 845

Gln Asp Gln Leu Ala Thr Val Lys Glu Thr Gln Lys Leu Ile Asp Leu 850 855 860

Glu Arg Ser Ala Leu Leu Glu Lys Gln Arg Glu Phe Ala Glu Asn Val 865 870 875 880

- Ala Gly Phe Lys Arg His Trp Ser Asn Lys Thr Ser Gln Leu Gln Lys 885 890 895
- Ile Tyr Glu Leu Thr Lys Lys Gln Glu Ser Glu Gln Thr Gln Lys Glu 900 905 910
- Thr Glu Leu Lys Ile Ala Phe Ser Asp Leu Gln Lys Asp Tyr Gln Val 915 920 925
- Phe Glu Leu Gln Lys Asp Gln Glu Phe Arg Gln Ile Glu Ala Lys Gln 930 935 940
- Arg Glu Leu Asp Lys Leu Ala Glu Lys Asn Asn Gln Val Lys Leu Glu 945 950 955 960
- Leu Asp Asn Arg Phe Gln Ala Leu Gln Asn Gln Lys Gln Asp Thr Val 965 970 975
- Gln Ala Gln Leu Glu Leu Glu Arg Glu Gln His Gln Leu Asn Leu Glu 980 985 990
- Gln Thr Ala Phe Asn Gln Ala Asn Glu Ser Leu Leu Lys Gln Arg Glu 995 1000 1005
- Gln Leu Thr Lys Lys Ile Gln Ala Phe His Tyr Glu Leu Lys Lys 1010 1015 1020
- Arg Asn Gln Phe Leu Ala Leu Lys Gly Lys Arg Leu Phe Ala Lys 1025 1030 1035
- Glu Gln Asp Gln Gln Arg Lys Asp Gln Glu Ile Asn Trp Arg Phe 1040 1045 1050
- Lys Gln Phe Glu Lys Glu Tyr Thr Asp Phe Asp Glu Ala Lys Lys 1055 1060 1065
- Arg Glu Leu Glu Glu Leu Glu Lys Ile Arg Arg Ser Leu Ser Gln 1070 1075 1080
- Ser Asn Val Glu Leu Glu Arg Lys Arg Glu Lys Leu Ala Thr Asp 1085 1090 1095
- Phe Thr Asn Leu Asn Lys Val Gln His Asn Thr Gln Ile Asn Arg 1100 1105 1110
- Asp Gln Leu Asn Ser Gln Ile Arg Gln Phe Leu Leu Glu Arg Lys 1115 1120 1125
- Asn Phe Gln Arg Phe Ser Asn Glu Ala Asn Ala Lys Lys Ala Phe 1130 1135 1140
- Leu Ile Lys Arg Leu Arg Ser Phe Ala Ser Asn Leu Lys Leu Gln 1145 1150 1155
- Lys Glu Ala Leu Ala Ile Gln Lys Leu Glu Phe Asp Lys Arg Asp

	1160					1165		•	'	1170				
Glu	Gln 1175	Gln	Lys	Lys	Glu	Leu 1180	Gln	Gln	Ala	Thr	Leu 1185	Gln	Leu	Glu
Gln	Phe 1190	Lys	Phe	Glu	Lys	Gln 1195	Asn	Phe	Asp	Ile	Glu 1200	Lys	Gln	Arg
Gln	Leu 1205	Val	Ala	Ile	Lys	Thr 1210	Gln	Cys	Glu	Lys	Leu 1215	Ser	Asp	Glu
Lys	Lys 1220	Ala	Leu	Asn	Gln	Lys 1225	Leu	Val	Glu	Leu	Lys 1230	Asn	Leu	Ser
Gln	Thr 1235	Tyr	Leu	Ala	Asn	Lys 1240	Asn	Lys	Ala	Glu	Tyr 1245	Ser	Gln	Gln
Gln	Leu 1250	Gln	Gln	Lys	Tyr	Thr 1255	Asn	Leu	Leu	Asp	Leu 1260	Lys	Glu	Asn
Leu	Glu 1265	Arg	Thr	Lys	Asp	Gln 1270	Leu	Asp	Lys	Lys	His 1275	Arg	Ser	Ile
Phe	Ala 1280	Arg	Leu	Thr	Lys	Phe 1285	Ala	Asn	Asp	Leu	Arg 1290	Phe	Glu	Lys
Lys	Gln 1295	Leu	Leu	Lys	Ala	Gln 1300	Arg	Ile	Val	Asp	Asp 1305	Lys	Asn	Arg
Leu	Leu 1310	Lys	Glu	Asn	Glu	Arg 1315	Asn	Leu	His	Phe	Leu 1320	Ser	Asn	Glu
Thr	Glu 1325	Arg	Lys	Arg	Ala	Val 1330	Leu	Glu	Asp	Gln	Ile 1335	Ser	Tyr	Phe
Glu	Lys 1340	Gln	Arg	Lys	Gln	Ala 1345	Thr	Asp	Ala	Ile	Leu 1350	Ala	Ser	His
Lys	Glu 1355	Val	Lys	Lys	Lys	Glu 1360	Gly	Glu	Leu	Gln	Lys 1365	Leu	Leu	Val
Glu	Leu 1370	Glu	Thr	Arg	Lys	Thr 1375	Lys	Leu	Asn	Asn	Asp 1380		Ala	Lys
Phe	Ser 1385	Arg	Gln	Arg	Glu	Glu 1390	Phe	Glu	Asn	Gln	Arg 1395	Leu	Lys	Leu
Leu	Glu 1400	Leu	Gln	Lys	Thr	Leu 1405		Thr	Gln	Thr	Asn 1410		Asn	Asn
Phe	Lys 1415	Thr	Lys	Ala	Ile	Gln 1420	Glu	Ile	Glu	Asn	Ser 1425	Tyr	Lys	Arg
Gly	Met 1430	Glu	Glu	Leu	Asn	Phe 1435	Gln	Lys	Lys	Glu	Phe 1440	Asp	Lys	Asn

Lys Ser Arg Leu Tyr Glu Tyr Phe Arg Lys Met Arg Asp Glu Ile 1450 Glu Arg Lys Glu Ser Gln Val Lys Leu Val Leu Lys Glu Thr Gln 1465 Arg Lys Ala Asn Leu Leu Glu Ala Gln Ala Asn Lys Leu Asn Ile 1480 1475 Glu Lys Asn Thr Ile Asp Phe Lys Glu Lys Glu Leu Lys Ala Phe 1495 Lys Asp Lys Val Asp Gln Asp Ile Asp Ser Thr Asn Lys Gln Arg 1505 1510 Lys Glu Leu Asn Glu Leu Leu Asn Glu Asn Lys Leu Leu Gln Gln 1525 Ser Leu Ile Glu Arg Glu Arg Ala Ile Asn Ser Lys Asp Ser Leu 1540 Leu Asn Lys Lys Ile Glu Thr Ile Lys Arg Gln Leu His Asp Lys 1555 1560 1550 Glu Met Arg Val Leu Arg Leu Val Asp Arg Met Lys Leu Ala Glu 1570 Gln Lys Tyr Gln Thr Glu Ile Asn Arg Leu Arg Thr Gln Thr Phe 1585 1580 Asp Ser Glu Lys Gln Asp Ile Lys Asn Phe Phe Pro Pro Leu Phe 1595 Lys Ile Asn Gly Asn Asp Met Ala Phe Pro Tyr Leu Tyr Pro Trp 1615 Leu Tyr Pro Gln Gln Lys Gln Asp Asp Asn Thr Leu Gln Ile Arg 1635 1625 Gln Leu Phe Glu Gln Gln Leu Gln Phe Met Gln Gln Arg Tyr Glu 1645 Asn Glu Leu Asn Glu Leu Arg Arg Gln Arg Asn Leu Leu Glu Lys 1660 1655 Lys Leu Asp Gln Ile Gln Leu Glu Ser Gln Leu Asn Asn Lys Gln 1670 1675 Ser Glu Phe Ser Lys Val Glu Ser Met Met Glu Lys Leu Leu Glu 1690 Lys Thr Glu Ser Arg Leu Asn Asp Phe Asp Gln Lys Ile Asn Tyr 1705 1710 1700

```
Leu Thr Lys Lys Val Asn Gln His Asn Thr Tyr Gln Pro Ser Ser
                        1720
                                             1725
Tyr Gln Pro Thr Pro Ser Tyr Gln Asp Ser Asp Lys Gln Gln Leu
    1730
                        1735
                                             1740
Leu Phe Arg Ile Gln Glu Leu Glu Lys Gln Asn Leu Phe Gln Gln
                        1750
Gln Phe Gln Pro Ala Pro Ala Val Val Gln Gln Pro Thr Ser Phe
                                             1770
    1760
                        1765
Ala Ala Pro Asn Ile Thr Lys Gln Gln Gln Ile Ala Gln Leu Asn
                        1780
Ala Glu Ile Asn Asn Ile Lys Arg Leu Ile Ala Gln Lys Ala Ala
    1790
                        1795
Ser Lys
   1805
<210> 74
<211> 74
<212> PRT
<213> M. genitalium
<220>
<221> misc feature
<223> hypothetical protein
<220>
<221> misc_feature
<223> gi | 1045811
<400> 74
Met Gln Tyr Ser Ala Leu Ile Pro Leu Phe Ile Leu Leu Ile Ser Leu
Val Leu Phe Cys Phe Ser Phe Arg Lys Asn Gln Ser Glu Asn Gln Ile
            20
                               25
Val Lys Ile Leu Phe Phe Ala Tyr Cys Ile Asp Phe Leu Ala Leu Ile
Leu Ala Val Met Leu Leu Thr Phe Leu Ser His Gly Leu Leu Ser Leu
                       55
```

Ala Ile Leu Ile Pro Val Leu Val Phe Gln 65 70

<210> 75 <211> 1033

```
<212> PRT
```

<213> M. pneumoniae

<220>

<221> misc\_feature

<223> MG328 homolog

<220>

<221> misc feature

<223> gi 1674046

<400> 75

Met Glu Phe Leu Glu Gln Glu Gly Gln Glu Val Leu Thr Lys Glu Ile 1 5 10 15

Lys Ala Gly Phe Cys Glu Ile Thr Pro Ser Ser Ile Thr Glu Gln Thr
20 25 30

Thr Lys Pro Gln Leu Asp Glu Thr Gln Leu Val Asp Glu Tyr Val His 35 40 45

Thr Lys Glu Leu Glu Thr Thr Pro Ile Pro Ile Ser Phe Ala Thr Lys 50 55 60

Glu Val Leu Phe Glu Glu Val Phe Asn Thr Pro Ser Thr Gln Gln Val 65 70 75 80

Asp Glu Ser Val Leu Val Asn Glu Tyr Ile Glu Leu Thr Gln Gln Ile 85 90 95

Lys Asn Ala Ser Glu Gln Val Ser Ser Asn His Thr His Lys Phe Ser 100 105 110

Val Ala Thr Glu Pro Ala Ala Thr Lys Ala Val Ser Glu Thr Met Leu 115 120 125

Leu Asp Asp Tyr Val Glu Met Val Glu Gln Asp Val Gln Ala Gln Thr 130 135 140

Ala Leu Pro Gln Ala Ala Leu Asp Pro Thr Val Ser Leu Thr Phe Ser 145 150 155 160

Ser Pro Ile Asp Ser Asn Ala Ile Leu Val Tyr Pro Glu Met Lys Val 165 170 175

Pro His Val Phe Asp Thr Val Ala Pro Thr Thr Thr Thr Val Pro Leu
180 185 190

Asp Gln Thr Gln Leu Leu Asp Glu Leu Val Glu Val Pro Val Leu Thr
195 200 205

His Thr Val Thr Pro Ala Pro Leu Gln Pro Lys Ala Ala Pro Thr Asn

210 215 220

	210														
Phe 225	Ala	Leu	Asp	Gln	Thr 230	Gln	Leu	Val	Asp	Glu 235	Leu	Val	Thr	Val	Pro 240
Leu	Thr	His	Thr	Leu 245	Val	Asn	Glu	Ser	Ala 250	Pro	Val	Thr	Pro	Val 255	Val
Val	Thr	Ser	Pro 260	Ala	Ala	Glu	His	Ser 265	Phe	Ser	Ile	Thr	Thr 270	Val	Asp
Lys	Ala	Asn 275	Leu	Thr	Asn	Ala	Leu 280	Ser	Gln	Thr	Val	Val 285	Ile	Lys	Pro
Ala	Glu 290	Asp	Ser	Ala	His	Gln 295	Ser	Ala	Val	Leu	Asp 300	Lys	Glu	Ile	Ala
Thr 305	Lys	Gln	Ala	Gln	Leu 310	Gln	Gln	Leu	Gln	Ala 315	Gln	Ile	Glu	Leu	Arg 320
Gln	Ala	Gln	Leu	Glu 325	Thr	Pro	Pro	Val	Thr 330	Tyr	Met	Gly	Val	Glu 335	Glu
Tyr	Lys	Leu	Leu 340	Pro	Val	Gln	Asp	Val 345	Val	Pro	Val	Gln	Pro 350	Thr	Val
Ser	Phe	Glu 355	Met	Thr	Leu	Leu	Gln 360	Glu	Gln	Leu	Asp	Lys 365	Ala	Leu	Lys
His	Asn 370	Ala	Ala	Leu	Gln	Ile 375	Gln	Leu	Glu	Glu	Gln 380	Leu	Ala	Lys	Pro
Leu 385	Gln	Tyr	Asp	Gln	Ser 390	Pro	Val	Leu	Gln	Glu 395	Arg	Ile	Glu	Leu	Leu 400
Gln	Asn	Gln	Asn	Thr 405		Leu	Thr	Gln	Glu 410	Leu	Asn	Glu	Leu	Gln 415	Gln
Lys	Leu	Phe	Lys 420	Ser	Gln	Asn	Asn	Ser 425	Leu	Leu	Leu	Ala	Arg 430	Leu	Glu
Glu	Glu	Asn 435	_	Thr	Leu	Lys	Gln 440	His	Leu	Gln	Asn	Asn 445		Pro	Glu

435 440 445

Ala Asn Gln Leu Asn Phe Val Leu Glu Lys Gln Leu Glu Gln Leu Gln 450 455 460

Gln Asp Lys His Ser Leu Thr Leu Gln Ile Glu Gln Tyr Lys Phe Asp 465 470 475 480

Ser Lys Lys His Gln Glu Gln Leu Ala Leu Ile Pro Ser Leu Arg Ser 485 490 495

Glu Ile Asn Ser Leu Glu Thr Glu Val Ile Ser Leu Lys Gln Thr Asn 500 505 510

Gln Arg Leu Ser Leu Ile Glu Arg Glu Asn Asn Phe Leu Lys Thr Glu 515 520 525

Ile Lys Gln Leu Arg Glu Thr Lys Leu Asn Asp Glu Asn Thr Lys Tyr 530 535 540

Arg Asn Leu Leu Lys Gln Tyr Glu Leu Met Arg Ala Asp Ser Asp Ala 545 550 555 560

Lys Leu Lys Glu Leu Glu His Glu Gln His Leu Ala His Gln His His 565 570 575

Gln Glu Gln Leu Ala Gln Leu Gln Arg His Asn Glu Ala Leu Val Lys 580 585 590

Glu Leu Asp Gln Val Lys Ala Thr Asn Phe Glu Leu Gly Leu Ala Ala 595 600 605

Gln Gly Phe Glu Gln Gln Lys Val Val Leu Glu Gln Lys Asn Ser Ser 610 615 620

Leu Leu Ala Ser Leu Gln Ala Ala Glu Glu Asn Val Gln Ala Leu Gly 625 630 635 640

Ile Thr Asn Ser Glu Leu Gln Asn Gln Leu Asn Val Leu Glu Phe Thr 645 650 655

His Lys Glu Lys Thr Ala Phe Asp Ser Lys Thr Leu Thr Leu Thr Lys 660 665 670

Gln Gln Leu Glu Gln Thr Gln Phe Asp Leu Ser Leu Thr Gln Glu Gln 675 680 685

Leu Ala Thr Phe Lys Gln Gln Asn Gln Ser Leu Thr Asp Lys Leu Met 690 695 700

Ala Ser Glu Thr Gln Leu Asn His Leu Gln Gln Ser Asp Glu Asn Leu 705 710 715 720

Thr Gln Leu Gln Thr Gln His Glu Leu Leu Gln Glu Ser Tyr Asn Lys
725 730 735

Leu Gln Asp Glu Ala Asn His Thr Gln Gln Gln Phe His Gln Ala Gln 740 745 750

Asn Glu Leu Asp Ala Ala His Gln Gln Leu Ala Leu Phe Lys Gln Asn 755 760 765

Asn Glu Glu Leu Thr Asp Lys Cys Ser Asn Ile Gln Asn Glu Leu His 770 775 780

Asp Leu Asn Arg Val Lys Thr Asn Trp Glu Asn Leu Asn Thr Glu His 785 790 795 800

- Asn Leu Leu Gln Asp Lys Tyr Ala Gln Gln Lys Glu Gln Met Gln His 805 810 815
- Glu His Ser Asn Leu Ala Gln Ile Gln Ala Glu His Glu Leu Leu Gln 820 825 830
- Glu Ser Tyr Asn Lys Val Lys Ala Glu Leu Asn Glu Ile Gln Ile Thr 835 840 845
- Asn Leu Asn Glu Ala Asn Ala Gln Tyr Gln Asp Leu Leu Ser Ala Tyr 850 855 860
- Glu Leu Gln Ser Asn His Asn Lys Leu Lys Gln Glu Leu Gln Val 865 870 875 880
- Leu Asn Gln Val Asn Leu Glu Lys Gln Gln Leu Ala Gln Lys Leu His 885 890 895
- Asn Thr His Gln Ser Leu Ser Gln Thr His Ala Glu Leu Thr Gln Leu 900 905 910
- Gln Ala Ala Tyr Asn Asn Leu Gln Ala Thr Pro Pro Val Ser Asp Glu 915 920 925
- Leu Leu Glu Gln Phe Asn Gln Val Gln Leu Glu Lys Gln Arg Leu Leu 930 935 940
- Gln Gln Asn Leu Ala Leu Val His Glu Leu Gln Tyr Phe Asn Glu Leu 945 950 955 960
- Asn Ser Ser Gln Thr His Glu Ile Lys Thr Lys Gln Asp Glu Thr Val 965 970 975
- Lys Glu Val Ile Ile Val Glu Lys Glu Ile Pro Val Pro Pro Glu Lys 980 985 990
- Lys Pro Arg Leu Lys Lys Arg Asp Ile Val Ile Glu Asn Lys Glu Asp 995 1000 1005
- Ala Leu Gly Lys Leu Ser Lys Lys Glu Arg Ile Gln Ala Tyr Ala 1010 1015 1020
- Glu Arg Leu Ala Lys Ile Asn Gly Lys Gln 1025 1030
- <210> 76
- <211> 22
- <212> PRT
- <213> M. pneumoniae
- <220>
- <221> misc\_feature
- <223> A05\_orf139 Protein

```
<220>
<221> misc_feature
<223> gi | 1673719
<400> 76
Met Arg Trp Cys Arg Gly Ser Pro Tyr His Trp Asn Leu Asp Arg Arg
Asn Pro Asp Phe Pro Ala
           20
<210> 77
<211> 103
<212> PRT
<213> M. pneumoniae
<220>
<221> misc_feature
<223> B01 orf103b Protein
<220>
<221> misc_feature
<223> gi|1673772
<400> 77
Met Ser Ser Val Phe Ser Lys Pro Asn Leu Lys Arg Pro Ser Phe Asp
                5
                                    10
Val Lys Asn Leu Thr Lys Pro Ser Arg Leu Leu Ser Ala Thr Leu Arg
Ser Ser Cys Ala Phe Leu Ser Ser Ala Ser Phe Phe Ala Cys Ser Leu
Cys Phe Phe Cys Cys Ser Ser Ile Ser Phe Cys Ser Leu Ala Ser Ser
Ser Ala Arg Leu Arg Tyr Ser Ser Ser His Ser Phe Phe Cys Trp Val
Leu Phe Ser Arg Ser Gly Leu Ala Tyr Ser Ser Ser Asn Leu Ser Ser
Lys Ser Ser Arg Leu Arg Ser
            100
<210> 78
<211> 112
<212> PRT
<213> M. pneumoniae
```

```
<220>
<221> misc_feature
<223> VXpSPT7 orf112 Protein
<220>
<221> misc feature
<223> gi 1674374
<400> 78
Met Ile Asp Arg Phe Phe Trp Ser Ile Leu Ser Phe Leu Leu Thr Asn
                                    10
Leu Val Phe Leu Phe Val Ala Phe Leu Ile Leu Ile Tyr Leu Ile
Ser Glu Ile Thr Gln Gln Phe Ala Phe Ala Phe Ile Ala Thr Ile Val
                            40
Phe Ile Ile Phe Tyr Asn Ile Leu Phe Leu Ser Tyr Leu Leu Thr Met
    50
Tyr Ile Lys Gly Leu Lys Gln Ile Glu Gln Lys Ser Arg Tyr Leu Leu
Leu Val Leu Asp Val Lys Ala Asp Glu Leu Leu Pro Phe Ser Phe Leu
Gly Ser Leu Arg Lys Ser His Met Leu Glu Glu Met Leu Leu Glu Gln
                                105
                                                    110
<210> 79
<211> 147
<212> PRT
<213> M. pneumoniae
<220>
<221> misc feature
<223> B01_orf147 Protein
<220>
<221> misc feature
<223> gi 1673775
<400> 79
Met Pro Ser Ser Ala Phe Lys Ile Asn Leu Ser Val Ser Pro Trp Phe
                                    10
Phe Cys Ser Thr Trp Ser Ser Leu Ile Cys Trp Pro Trp Thr Ile Thr
```

```
Thr Ser Val Ser Arg Ser Thr Leu Ser Ser Thr Thr Trp Ile Leu Trp 35 40 45
```

Thr Trp Leu Phe Asn Ser Val Ser Ile Phe Val Ser Arg Trp Ser Phe 50 55 60

Asp Phe Leu Tyr Ser Leu Asn Ser Leu Arg Val Thr Tyr Ser Val Phe 65 70 75 80

Thr Gly Ile Thr Gly Leu Leu Ser Leu Asn Cys Leu Leu Lys Leu Pro 85 90 95

Glu Asn Ser Thr Leu Leu Leu Ser Leu Ser Ile Ile Tyr Gln Pro Glu 100 105 110

Lys Val Pro Phe Trp Ser Phe Ser Pro Cys His Glu Ile Leu Phe Arg 115 120 125

Tyr Lys Thr Glu Phe Ser Leu Ser Leu Ser His Thr Ser Phe Leu Phe 130 135 140

Ser Glu Ile

145

<210> 80 <211> 217

<211> 217
<212> PRT

<213> M. tuberculosis

<220>

<221> misc\_feature

<223> hypothetical protein Rv3611

<220>

<221> misc\_feature <223> gi|2113965

<400> 80

Met Ala Ile Ala Asn Pro Ala Glu Pro Gly Ala Ala Gly Arg His His 1 5 10 15

Gln Pro Arg Gly Asp Arg Lys Pro Arg Ala Trp Arg Gln Cys Gly Pro
20 25 30

Gln Asn Gly Pro Arg Arg Ser Gln Ala Ile Thr Pro Glu Pro Gly Ala 35 40 45

Ala Gly Arg His His Gln Pro Arg Gly Asp Arg Lys Pro Arg Ala Trp 50 55 60

<211> 73

```
Arg Gln Cys Gly Pro Gln Asn Gly Pro Arg Arg Ser Gln Ala Ile Thr
                    70
Pro Glu Pro Gly Ala Ala Gly Arg His His Gln Pro Arg Gly Asp Arg
Lys Pro Arg Ala Trp Arg Gln Cys Gly Pro Gln Asn Gly Pro Arg Arg
Ser Gln Ala Ile Thr Pro Glu Pro Gly Ala Ala Gly Arg His His Gln
                            120
        115
Pro Arg Gly Asp Arg Lys Pro Arg Ala Trp Arg Gln Cys Gly Pro Gln
                        135
Asn Gly Pro Arg Arg Ser Gln Ala Ile Thr Pro Glu Pro Gly Ala Ala
145
                    150
Gly Arg His His Gln Pro Arg Gly Asp Arg Lys Pro Arg Ala Trp Arg
                                    170
Gln Cys Gly Pro Gln Asn Gly Pro Arg Arg Ser Gln Ala Ile Thr Pro
Glu Pro Gly Ala Ala Gly Arg His Trp Leu Asp Gln Arg Pro Val Val
                            200
Pro Asp Gly Val Gly Lys Ser Asp Ser
<210> 81
<211> 27
<212> PRT
<213> M. tuberculosis
<220>
<221> misc feature
<223> hypothetical protein Rv1572c
<220>
<221> misc feature
<223> gi 2117265
<400> 81
His Gly Gln Pro Arg Thr Asn Thr Phe His His Glu Lys Leu Leu
                5
Arg His Asn Asp Glu Asp Asn His Asp Asp Pro
<210> 82
```

```
<212> PRT
<213> M. tuberculosis
<220>
<221> misc feature
<223> hypothetical protein Rv0378
<220>
<221> misc feature
<223> gi 2909499
<400> 82
Met Ser Gly Arg Trp Glu Ala Gly Asn Ala Asp Gly Asn Gly Gly Ser
                5
Ala Gly Leu Ile Gly Ser Gly Gly Ala Gly Gly Asp Gly Gly Ser Gly
Gly Ala Thr Gly Ala Gly Gly Glu Gly Gly Asp Ala Gly Ala Ser Gly
Ser Ile Asn Gly Asn Ala Gly Asp Pro Gly Asn Ser Gly Glu Arg Gly
    50
Ala Val Gly Lys Pro Gly Ala Pro Gly
                    70
<210> 83
<211> 47
<212> PRT
<213> N. meningitis MC58
<220>
<221> misc feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi | 7225315
<400> 83
Met Glu Trp Ala Glu Asn Glu Thr Val Lys Leu Ala Gln Lys Trp Glu
Gln Glu Gln Lys Lys Gln Gln Ile Gln Gln Lys Lys Glu Thr Glu Lys
            20
Ser Pro Lys His Lys Ala Ser Arg Asp Asp Trp Glu Met Glu Arg
                            40
        35
```

```
<210> 84
<211> 107
<212> PRT
<213> N. meningitis MC58
<220>
<221> misc feature
<223> hypothetical protein
<220>
<221> misc_feature
<223> gi 7226708
<400> 84
Met Lys Lys Leu Leu Ile Ala Ala Met Met Ala Ala Ala Leu Ala Ala
Cys Ser Gln Glu Ala Lys Gln Glu Val Lys Glu Ala Val Gln Ala Val
Glu Ser Asp Val Lys Asp Thr Ala Ala Ser Ala Ala Glu Ser Ala Ala
Ser Ala Val Glu Glu Ala Lys Asp Gln Val Lys Asp Ala Ala Asp
Ala Lys Ala Ser Ala Glu Glu Ala Val Thr Glu Ala Lys Glu Ala Val
                   70
Thr Glu Ala Ala Lys Asp Thr Leu Asn Lys Ala Ala Asp Ala Thr Gln
Glu Ala Ala Asp Lys Met Lys Asp Ala Ala Lys
           100
<210> 85
<211> 98
<212> PRT
<213> N. meningitis MC58
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi 7226768
<400> 85
```

Met Lys Lys Ser Leu Phe Ala Ala Ala Leu Leu Ser Leu Val Leu Ala

Ala Cys Gly Glu Lys Ala Ala Glu Ala Pro Ala Ala Glu Ala Pro 20 25 30

Ala Ala Glu Ala Pro Ala Thr Glu Ala Pro Ala Ala Glu Ala Pro Ala 35 40 45

Ala Glu Ala Pro Ala Ala Glu Ala Pro Ala Ala Glu Ala Ala Thr 50 55 60

Glu Ala Pro Ala Ala Glu Ala Ala Ala Thr Glu Ala Pro Ala Ala Glu 65 70 75 80

Ala Ala Ala Thr Glu Ala Pro Ala Ala Glu Ala Pro Ala Ala Glu Ala 85 90 95

Ala Lys

<210> 86

<211> 34

<212> PRT

<213> N. meningitis MC58

<220>

<221> misc\_feature

<223> hypothetical protein

<220>

<221> misc feature

<223> gi 7227030

<400> 86

Met Pro Trp Lys Ile Ser Thr Thr Thr Asn Leu Thr Pro Val Pro Ser 1 5 10 15

Ala Asn Leu Ser Ala Leu Pro Thr Thr Arg Cys Thr Thr Pro Pro Pro 20 25 30

Thr Pro

<210> 87

<211> 114

<212> PRT

<213> N. meningitis MC58

<220>

<221> misc\_feature

```
<223> hypothetical protein
<220>
<221> misc feature
<223> gi | 7227104
<400> 87
Met Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro
Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly
            20
Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser
Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro
    50
Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly
                    70
Ile Pro Glu Ser Ser Gly Ile Pro Glu Ser Ser Gly Ile Pro Glu Pro
Ser Phe Pro Arg Arg Glu Ser Arg Pro Val Gly Ala Glu Thr Tyr
Arg Val
<210> 88
<211> 120
<212> PRT
<213> N. meningitis MC58
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi 7226645
<400> 88
Met Ile Ala Lys Ser Leu Phe Phe Arg Cys Gln Lys Ile Tyr Phe Ile
Tyr Phe Ile Leu Phe Ile Cys Leu Tyr Leu Asn Ile Ser Tyr Asp Gly
```

20

```
Glu Ile Phe Ile Tyr Phe Ile Ile Asn Phe Thr His Leu Leu Ile Cys
His Gly Ile Leu Leu Val Phe Cys Arg Ile Phe Pro Tyr Glu Asn Ile
Pro Phe Thr Ile Phe Leu Asn Phe Ile Ser Leu Phe Leu Ile Phe Leu
Pro Leu Ile Phe Thr Ile Arg Glu Leu Ile Asp Ser Tyr Tyr Ile Glu
Ser Ile Ile Asn Leu Phe Leu Ile Leu Ile Pro His Val Ile Phe Leu
                                105
Ile Tyr Leu Lys Gly Lys Gln Ile
<210> 89
<211> 78
<212> PRT
<213> Pseudomonas aeruginosa
<220>
<221> misc_feature
<223> AE004587 5 hypothetical protein
<220>
<221> misc feature
<223> gi|9947556
<400> 89
Met Lys Lys Thr Val Thr Leu Ala Leu Leu Leu Ala Ala Ser Leu Gly
Leu Ala Ala Cys Asp Lys Lys Glu Glu Asp Lys Ala Ala Ala Pro Ala
Ala Pro Ala Thr Glu Thr Gln Pro Ser Ala Pro Ala Thr Pro Pro Ala
Glu Pro Ser Ala Pro Ala Pro Ser Ser Asp Thr Pro Ala Thr Pro Gln
```

Thr Pro Ala Pro Thr Pro Glu Gln Pro Gln Gln Asn Gln Gln

70

<210> 90 <211> 52 <212> PRT

THE WAS THE THE WAS THE

#

```
<213> Pseudomonas aeruginosa
<220>
<221> misc_feature
<223> AE004746 3 hypothetical protein
<220>
<221> misc feature
<223> gi | 9949353
<400> 90
Met Ser Leu Gly Thr Ile Leu Leu Ile Ile Leu Ile Leu Leu Leu Ile
Gly Gly Leu Pro Val Phe Pro His Ser Arg Asn Trp Gly Tyr Gly Pro
                                                    30
Ser Gly Ile Ile Gly Ala Leu Leu Val Val Leu Leu Val Leu Leu Leu
Leu Gly Met Ile
   50
<210> 91
<211> 126
<212> PRT
<213> Pseudomonas aeruginosa
<220>
<221> misc_feature
<223> AE004708_10 hypothetical protein
<220>
<221> misc feature
<223> gi 9948900
<400> 91
Met Leu Lys Leu Phe Ala Thr Gly Leu Ala Ala Ser Phe Leu Leu
                5
Pro Pro Ala Gln Ala Ala Pro Pro Ala Pro Tyr Gly Val Gln Pro His
Gln Gln Ala Val Gln Arg Ala Gly Glu Gln Arg Gln Arg Gln Leu Gln
Glu Gln Arg Gln Arg Phe Asp Glu Gln Arg Leu Gln Leu Gln Gln Asp
                        55
```

Gln Leu Gln Arg Gln Gln Gln Asn Leu Gln Arg Gln Arg Gln Arg Gln Arg Gln Arg Gln Arg Gln Met Gln Asp Asn Leu Ile Arg Gln Gln Gln Leu Asp Gln Gln Arg

85 90 95

Trp Arg Leu Glu Gln Asp Gln Arg Arg Leu Asp Ser Glu Arg Arg Gln
100 105 110

Leu Glu Asn Arg Arg Arg Gln Ser Gln Ser Pro Ala Ile Arg 115 120 125

<210> 92

<211> 101

<212> PRT

<213> Pseudomonas aeruginosa

<220>

<221> misc\_feature

<223> AE004643\_2 hypothetical protein

<220>

<221> misc\_feature

<223> gi 9948180

<400> 92

Met Ser Ala Asp Glu Lys Arg Ile Arg Glu Phe Ala Tyr Gln Ile Trp 1 5 10 15

Glu Ser Glu Gly Cys Pro Asp Gly Gln Ala Glu Arg His Trp Ala Met

Ala Arg Gln Leu Ala Glu Ala Glu Ala Ala Ala Ala Pro Lys Lys 35 40 45

Thr Arg Gly Arg Ala Lys Ala Ala Lys Glu Thr Pro Ala Leu Leu Gln
50 55 60

Ala Pro Ala Ala Lys Pro Arg Lys Pro Arg Ala Ala Ser Pro Ala Arg 65 70 75 80

Pro Ala Ser Glu Lys Pro Ala Ala Ala Lys Pro Arg Ser Arg Lys 85 90 95

Pro Glu Ala Gly Glu 100

<210> 93

<211> 521

<212> PRT

<213> R. prowazekii

```
<220>
<221> misc feature
<223> unknown
<220>
<221> misc feature
<223> gi|3860652
<400> 93
Met Lys Lys Glu Ile Leu Ser Lys Gln Gly Asn Ile Leu Glu Gln Leu
                                    10
Lys Phe Ile Asn Ala Asn Thr Glu Ile Leu Thr Glu His Ser Lys Ala
            20
Ile Leu Lys Asp Lys Leu Lys Glu Leu Ser Lys Gln Leu Asp Glu Ile
Ser Ser Asn Lys Leu Val Gly Phe Ile Leu Asp Glu Asn Lys Ile Asn
Thr Asn Phe Lys Asn Val Pro Phe Ser Glu Lys Lys Val Arg Glu Gln
Val Asn Asn Leu Asn Asn Lys Ile Leu Glu Lys Ile Phe Leu Lys Asp
Asp Gly Thr Ile Thr Glu Gln Asp Leu Thr Lys Ile Leu Gln Lys His
Lys Glu Thr Val Leu Ile Lys Asn Leu Thr Lys Ala Ile Val Tyr Ile
Asp Gly Asn Lys Asn Asn Glu Thr Val Asn Lys Thr Leu Glu Lys Cys
                        135
Leu Glu Glu Thr Thr Pro Glu Gln Gln Gly Met Ile Leu Asp Val Leu
                    150
145
Thr Asn Asn Thr Arg Ile Arg Lys Ala Leu Ile Thr Lys Ile Glu Arg
                                    170
Glu Gln Arg Gln Glu His Asn Gln Lys Leu Asn Lys Asn Ile Ala Gly
                                185
Asp Thr Phe Val Asp Ala Leu Lys Lys Ala Leu Val His Arg Thr Ser
        195
Asn Pro Glu Thr Ile Gln Lys Ser Leu Glu Arg Arg Lys Lys Glu Thr
```

Pro Lys Asn Leu Asn Val Trp Asp Arg Ile Ser Gln Asn Ile Pro Asn

225 230 235 240

Leu Asn Asn Gln Asn Asp Asn Gln Asn Gly Gln Asp Glu Asn Asn Lys
245 250 255

Glu Trp Glu Glu Ser Asn Gln Asn Ala Asp Tyr Leu Asn Asn Thr Asn 260 265 270

Ile Tyr Arg Ile Thr Lys Ala Lys Gln Asp Leu Glu Lys Ala Val Lys 275 280 285

Glu Thr Ile Asn Lys Phe Ser Ala Met Ser Thr Leu Ile Lys Asp Asn 290 295 300

Thr Ile Lys Asn Thr Met Ala Tyr Gln Lys Tyr Leu Lys Gly Ala Glu 305 310 315 320

Asp Gln Leu Ala Leu Ala Lys Glu Lys Gly Lys Glu Leu Ile Glu Asn 325 330 335

Ser Val Gln Thr Phe Lys Ile Ile Pro Lys Lys Tyr Gln Asp Asp Met 340 345 350

Asn Glu Asn Trp Gln Asn Tyr Leu Ser Pro Glu Glu Ile Ile Glu Leu 355 360 365

Thr Ala Leu Asn Glu His Thr Asn Thr Leu Thr Ser Asn Lys Asn Lys 370 375 380

Ser Gly Tyr Phe Thr Ser Thr Ala Glu Ala Leu Gln Cys Lys Thr Lys 385 390 395 400

Gln Gln Glu Tyr Tyr Thr Leu Leu Ser Lys Leu Lys Lys Ile Gly Ile 405 410 415

Glu Lys Gln Gln Lys Lys Leu Val Lys Asp Tyr Val Asp Glu Met Ile 420 425 430

Thr Asn Ala Lys Gln Ala Val Lys Lys Ile Glu Arg Thr Leu Glu Lys 435 440 445

Val Asn Gln Lys Lys Glu Asn Lys Tyr Glu Phe Ser Glu Ser Ser Ala 450 455 460

Leu Ile Ser Lys Glu Ile Leu Asp Ala Gln Ala Arg Leu Glu Asn Ala 465 470 475 480

Lys Gln Lys Ile Glu Phe Ile Lys Leu Lys Gln Ile Ile Ser Asp Lys 485 490 495

Arg Gln Val Asn Ser Ser Asp Glu Asp Ser Asp Asp Ser Lys Lys 500 505 510

Lys Cys Asn Gln Thr Lys Ser Arg Thr 515 520 <210> 94 <211> 143 <212> PRT <213> R. prowazekii

<220>
<221> misc\_feature
<223> unknown

<220>

<221> misc\_feature <223> gi|3860651

<400> 94

Met Lys Ile Gln Met Met Ile Leu Lys Lys Asn Ala Ile Lys Leu Lys 1 5 10 15

Val Glu Leu Glu Asn Ala Gln Lys Asp Ile Asn Gln Ala Lys Lys Asn 20 25 30

Leu Glu Asn Ala Glu Ala Lys Asn Glu Ala Leu Gln Arg Gln Ile Ile 35 40 45

Leu Asn His Asn Gln Asn Glu Val Asn Ser His Thr Thr Lys Asn Gln 50 55 60

Glu Lys Phe Lys Thr Asp Asn Val Thr Glu Glu Tyr Leu Glu Asp Met 65 70 75 80

Ala Leu Met Phe Lys Asn Ser Glu Asp Thr Ala Glu Gln Lys Glu Glu 85 90 95

Val Asn Cys Gln His His Glu Glu Gln Asn Arg Gln Lys Gln Glu His
100 105 110

Ile Asn Thr Glu Glu Glu Ala Val His Lys Glu Lys Ile Ile His Ile
115 120 125

Thr Glu Glu Thr Glu Thr Glu Ala Phe Lys Lys Glu Ile Asp Leu 130 135 140

<210> 95 <211> 369

<212> PRT

<213> T. pallidum

<220>

<221> misc\_feature

<223> conserved hypothetical protein

<220>
<221> misc\_feature
<223> gi|3322751

<400> 95

Met Cys Gln Lys Ser Ser Pro Cys Thr Tyr Ala Arg Val Arg Ser Leu 1 5 10 15

Pro Ser Val Arg Leu Phe Ser Phe Leu Ala Leu Ala Phe Ala Ser Phe 20 25 30

Leu Arg Ala Glu Asp Ala Phe Asp His Phe Arg Glu Gly Glu Arg Leu 35 40 45

Leu Ser Leu Gln Gln Ala Gln Gln Ala Ile Gly Pro Leu His Lys Ala 50 55 60

Ala Gln Gln Lys Pro Ala His Pro Lys Ala Ala Leu Tyr Leu Gly Met 65 70 75 80

Ala Tyr Leu Gln Thr Gly Arg Tyr Thr Gln Ala Ile Gln Trp Leu Gln 85 90 95

Asn Pro Pro Val His Ser Gln Glu Tyr Ala His Leu Tyr Ala Tyr Asn 100 105 110

Leu Gly Asn Val Tyr Phe Val Gln His Arg Tyr Glu Glu Ala Gln His 115 120 125

Ala Tyr Glu Gln Ala Leu Ala Leu Lys His Asp Tyr Pro Pro Ala Leu 130 135 140

Leu Ala Asp Tyr Lys Lys Tyr Val Ser Gln Asn Pro Thr Ala Ser Gln
165 170 175

His Tyr Glu Val Gln Arg Met Ile Ala Ala Leu Glu Gln Trp Leu Gln 180 185 190

Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg 195 200 205

Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg

Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg 225 230 235 240

Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg 245 250 255

```
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg
            260
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg
                            280
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Glu Ala Arg
                    310
Arg Lys Glu Ala Glu Glu Ala Arg Arg Lys Glu Ala Glu Phe Glu Ala
                                    330
Leu Lys Arg Ala Leu Arg Leu Lys Gln Ala Glu Asp Ala Arg Thr Leu
                                345
            340
Ser Thr Gly Ser Glu Asp Thr Val Pro Tyr Gln Glu Glu His Asn Leu
                            360
Glu
<210> 96
<211> 41
<212> PRT
<213> T. pallidum
<220>
<221> misc feature
<223> predicted coding region TP0266
<220>
<221> misc_feature
<223> gi 3322546
<400> 96
Met Val Arg Val Gln Arg Arg Val Leu Lys Asn Phe Met Arg Val Val
Gly Val Asp Lys Gly Tyr Arg Leu Trp Val Glu Trp Leu Ser Cys Val
```

Cys Cys Gly Tyr Val Val Arg Ala Glu

<210> 97 <211> 38 <212> PRT

<213> Vibrio cholerae

```
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi | 9654409
<400> 97
Met Ser Lys Gln Glu Met Lys Lys Pro Gln Leu Ser Leu Lys Glu Lys
Arg Lys Leu Lys Gln Glu Lys Ala Gln Glu Ser Ser Val Ile Lys Pro
            20
Arg Lys Ser Lys Gly Arg
        35
<210> 98
<211> 85
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi | 9654544
<400> 98
Met Phe Leu Ser Phe Ile Cys Phe Tyr Ile Phe Lys Asn Gly Ser Tyr
Phe Ser Phe Ile Cys Leu Val Gly Cys Phe Gln Phe Phe Asp Phe Phe
            20
Val Val Phe Ile Gly Phe Leu Phe Leu Phe Cys Ser Phe Gly Leu
Val Asp Phe Ser Phe Phe Tyr Phe Val Leu Ile Val Phe His Leu Phe
Gly Val Asp Leu Leu Ser Trp Phe Gly Trp Trp Gln Val Phe Leu Phe
                                        75
                    70
Cys Asn Phe Ile Glu
                85
```

```
<210> 99
<211> 43
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc feature
<223> hypothetical protein
<220>
<221> misc_feature
<223> gi|9654912
<400> 99
Met Leu Asn His Leu Leu Val Arg Leu Thr Ile Gly Cys Leu Leu Val
Leu Gly Ile Lys Leu Ser Ala Leu Tyr Phe Leu Pro Met Val Leu Leu
Leu Asn Thr His His Lys Glu Phe Phe Gly Trp
<210> 100
<211> 31
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc_feature
<223> gi|9656707
<400> 100
Met Pro Arg His Pro Phe Val Phe Val Val Ile Pro Lys Pro Pro Phe
Leu Ala Val Val Ile Val Leu Arg Phe Val Val Thr Arg Tyr Leu
<210> 101
<211> 88
<212> PRT
<213> Vibrio cholerae
```

Asn

```
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc feature
<223> qi | 9657609
<400> 101
Met Leu Ser Leu Ala Val Pro Leu Leu Phe Met Ser Leu Leu Gly Phe
                                    10
Lys Leu Lys Leu Pro Tyr Gly Leu Leu Met Gly Leu Ile Ile Leu Thr
                                25
            20
Leu Leu Gly Trp Leu Gly Asn Val Ser Leu Leu Pro Val Leu Val
Val Leu Phe Phe Met Ser Pro Leu Leu Leu Ala Thr Lys Arg Ala Pro
Trp Gln Ser Ile Leu Phe Gly Val Gly Cys Leu Leu Pro Gln Leu Val
Gln Phe Val Met Leu Asn Gln Arg
<210> 102
<211> 33
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi | 9657724
<400> 102
Met Arg Arg Leu Leu Cys Leu Ser Phe Asn Thr Leu His Leu Asn Gln
Ile Asn Asp Asn Gln Leu Lys Ser Leu Thr Lys Leu Arg Ile Ile Leu
            20
```

```
<210> 103
<211> 34
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc feature
<223> hypothetical protein
<220>
<221> misc_feature
<223> gi 9657931
<400> 103
Met Gly Lys Ser Met Pro Ile Gln Leu Leu Leu Leu Ser Ile Pro Phe
Leu Leu Asp Ala Ala Thr Pro Ser Arg Leu Gly Ile Lys Ile Leu Ile
Leu Lys
<210> 104
<211> 36
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc_feature
<223> gi|9658035
<400> 104
Met Gly Tyr Pro Ser Met Ala Ala Ala Leu His Ala Ala Ala Leu Asn
Ile Ala Leu Asn Ile Gln Leu Asn Ile Ser Met Arg Ala Met Leu Leu
Ala Phe Leu Glu
        35
<210> 105
<211> 38
```

```
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc feature
<223> hypothetical protein
<220>
<221> misc feature
<223> gi 9658254
<400> 105
Met Leu Ile Arg Glu Leu Ala Leu Ala Ala Tyr Gln Phe His Arg Tyr
                                                        15
                5
Phe Lys Ile His Phe Met Phe Gln Phe Lys Val Phe Leu Phe Leu Ala
Lys Gly Phe Phe Ser Phe
        35
<210> 106
<211> 35
<212> PRT
<213> Vibrio cholerae
<220>
<221> misc_feature
<223> hypothetical protein
<220>
<221> misc_feature
<223> gi 9656580
<400> 106
Met Lys Leu Asn Asp Leu Asn Lys Lys Pro Leu Val Ile Lys Lys Thr
                5
Ala Leu Ser Phe Gln Lys Leu Lys Lys Leu Gln Gln Pro Val Lys Lys
                                25
Phe His Phe
        35
<210> 107
<211> 665
<212> PRT
<213> Plasmodium falciparum
```

<220>
<221> misc\_feature
<223> hypothetical protein

<220>
<221> misc\_feature

<400> 107

<223> qi 3845248

Met Gln Tyr Phe Phe Leu Val Phe Leu Ala Val Leu Ala Lys Gly Phe 1 5 10 15

Leu Arg Asn Lys Glu His Ala Asn Leu Ile Asn Ser Tyr Asn Asp Ile
20 25 30

Val Glu Asp Ile Asn Ile Lys Lys Glu Glu Lys Ser Ser Glu Pro 35 40 45

Pro Phe Ile Pro Ile Lys Asn Lys Ile Asp Asn Val His Thr Lys Asn 50 55 60

Asn Asn Gln Tyr Asn Leu His Asn Asn Lys Ser Asn Lys Thr His Leu 65 70 75 80

Thr Tyr Gly Thr His Thr Ser Phe Leu Gln Asn Cys Thr Ile Asn Asp 85 90 95

Cys Val Asp Val Asp Asn Lys Asp Ser Glu Ile Asn Asn Ile Thr Lys 100 105 110

Glu Lys Asp Asp Asn Asn Asn Asn Gly Thr Lys Gln Ile Glu Glu
115 120 125

Lys Asn Lys Ile Asn Lys Ser Asp Leu His Arg Gln Asn Glu Leu Asn 130 135 140

Leu Gln Ser Gly Lys Asn Glu Gln Asp Ile Asn Lys Asn Glu Lys Gly
145 150 155 160

Lys Gln Asp Ile Ser Asn Ser Asn Ala Glu Asn Lys Lys Asp Val Lys 165 170 175

Glu Gly Val Lys Glu Leu Glu Glu Lys Lys Lys Glu Glu Lys Ile Ser 180 185 190

Asp Asp His Lys Val Glu Glu Asn Lys Lys Ser Asp Asp His Lys Val 195 200 205

Glu Glu Asn Lys Lys Ser Asp Asp His Lys Val Glu Glu Asn Lys Lys 210 215 220

Ser Asp Asp His Lys Ile Glu Glu Val Lys Lys Val Glu Glu His Glu

225 230 235 240

Glu Asp Glu Glu Glu Asp Lys Lys Glu Lys Lys Ser Glu Asn Lys Asn
245
250
255

Lys Asp Glu Asn Lys Asp Glu Asn Asp Glu Asp Asn Asp Glu Ile Ser 260 265 270

Asp Glu Asp Glu Val Asp Asp Asp Val Glu Glu Asp Lys Asn Glu Asn 275 280 285

Asp Asp Ile Asp Asp Asp Lys Lys Glu Thr Asp Lys Thr His Leu Glu 290 295 300

Glu Glu Glu Asn Glu Ile Ile Glu Lys Glu Phe Ser Asp Lys Lys 305 310 315 320

Asn Gly Lys Asn Lys Asp Thr Lys Lys Glu Lys Ser Lys Asp Thr Glu 325 330 335

Lys Glu Lys Ser Lys Asp Ile Glu Lys Glu Lys Ser Lys Asp Lys Glu 340 350

Lys Glu Lys Ser Lys Asp Lys Glu Lys Glu Lys Gly Lys Asp Lys Glu 355 360 365

Lys Glu Lys Ser Lys Asp Ile Glu Lys Glu Lys Glu Lys Asp Lys Asp 370 375 380

Ile Glu Lys Glu Lys Ser Lys Asp Thr Ala Lys Glu Lys Glu Lys Asp 385 390 395 400

Lys Asp Ile Glu Lys Glu Lys Ser Lys Asp Met Glu Lys Leu Lys Asn
405 410 415

Lys Gln Asn Asp Glu Lys Lys Lys Asp Asp Asn Glu Lys Lys Asn 420 425 430

Asp Lys Gln Asp Ile His Asp Asp Asn Asp Glu Asn Asp Met Glu
435 440 445

Glu Ile Glu Glu Asn Asp Asp Glu Glu Asp Glu Asp Glu Asp Met Glu
450 460

Asn Lys Lys Lys Lys Lys Gly Lys Asn Gly Asn Glu Asn Gly Asn 465 470 475 480

Glu Asn Gly Ser Glu Asn Gly Asn Glu Asn Gly Asn Glu Asn Gly Asn 485 490 495

Glu Asn Glu Asn Lys Asn Glu Ser Glu Asn Glu Asn Glu Asn Glu Asn 500 505 510

Glu Asn Glu Asn Gly Asn Glu Asn Glu Asn Glu Lys 515 520 525

Asp Lys Asn Ile Lys Glu Ile Glu Asn Val Thr Asn Ala Asn Lys Glu 530 535 540

Asn Tyr Glu Lys Ile Asn Lys Asn Ser Glu Ile Thr Ile Thr Lys Ser 545 550 555 560

Asn Ile Asp Ile Tyr Asn Asn Asn Arg Asn Asn Asp Ile Asp Lys Val 565 570 575

Asn Asn His Ile Phe Thr Asn Gln Gln Lys Lys His Asn Leu His Asn 580 585 590

Glu Gln Asn Lys Phe Asn Glu Thr Leu Asn Val Ser Thr Asn His Lys 595 600 605

Asn His Tyr Glu Glu Lys Lys Lys Tyr Glu Ser Asn Met Phe Asn Val 610 615 620

Asp Lys Arg Met His Lys Asn Leu Thr Ser Met Asp Thr Ile Leu His 625 630 635 640

Asn Leu Asn Asp Lys Leu Ser His His Lys Asp Leu Lys Asn Val Leu 645 650 655

Asn Asp Lys Lys Lys Lys Asn Lys 660 665

<210> 108

<211> 807

<212> PRT

<213> Plasmodium falciparum

<220>

<221> misc feature

<223> hypothetical protein

<220>

<221> misc\_feature <223> qi|3845292

<400> 108

Met Ala Val Glu Ser Lys Pro Asn Asn Ser Ser Lys Glu Lys Asn Glu
1 5 10 15

Glu Asn Asp Ile Ile Asn Lys Cys Asp Asp Ser Asn Lys Ile Asn Gly
20 25 30

Lys Glu Asn Ile Phe Ala Val Glu Lys Val Gly Ile Asn Glu Ser Gly 35 40 45

His Met Ser Asn Asp Asn Ile Asn Lys Asn Gln Glu Lys Asn Lys

50 55 60

Lys Lys Lys Lys Lys Asn Thr His Lys Lys Val Asn Ile Asn Asn Thr 70 75 His Ile Asn Ile His Thr Thr Asn Asp Lys Asn Asn Gly Gln Asp Ile Asn Lys Pro Glu Val Ile Glu Arg Asp Asn Ile Ile Asn Ile Lys Asn 105 Asp Thr Asn Asn Ile Leu Asp Ser Ser Tyr Asn Glu Glu Gly Asn Glu 115 Asn Asn Arg Asn Asp Ile Asn Asn Asn Asn Asn Asn Asn Ile Asn 135 Ile Asn Asn Asn Ile Asn Asn Ser Cys Ser Asn Asn Tyr Gly Leu 150 155 145 Lys Lys Lys Ile Thr Leu Leu Lys Arg Asn Asp Ile Lys Asp Glu Gly 165 Tyr Asn Asn Glu Asn Ile Thr Thr Leu Asn Asn Lys Asn Asn Leu Lys 185 Asn Asn Asn Tyr Asn Asp Asn Arg Asn Asn Asn Asn Asn Asn Lys 195 200 Asn Asn Ile Asn Asn Asn Asn Asn Asn Cys Cys Ser Glu Lys Thr 215 Leu Glu Gln Arg Glu Lys Glu Tyr Asn Lys Ile Arg Ala Arg Ile Phe 235 230 Ser Asn Phe Asn Lys Lys Gln Lys Asn Val Gln Lys Thr Glu Gln Asn 250 245 Asn Leu Asn His Thr Tyr Leu Asn Asn Asn Ile Ile Asn Asn Ile Asn 265 Asn Gly Asp Asn Gln Tyr Ala Tyr Ile Asn Asn Phe Tyr His Ile Tyr His Asn Asn Ser Tyr Asn His Ile Tyr Arg Gln Asn Asn Ile Pro Ile

Cys Asn Ile Asn Asn His Ala Pro Asn Ile Glu Lys Leu Asn Asn Pro 305 310 315 320

Tyr Tyr Tyr His Asp Asn His Ile Ala Tyr Thr Asn Tyr Met Tyr Ser

325

Thr Gln Asn Lys Met Asn Asn Met Lys Thr Lys Gln Ile Gly His Tyr 340 345 350

330

625

Gly Ile Asn Asn Glu Asp Asn Asn Asn Asn Asn Asn Asn Asn Ile Asn 360 Asn Asn Asn Asn Asn Ile Asn Asn Asn Ile Asn Asn Asn Asn 375 Val Pro Leu Cys Ile Pro Gln Leu Asp Asn Tyr Asn Lys Thr Lys Asn 390 Asn Phe Asn Gln Gly Thr Asn Asn Phe Asn Gln Gly Thr Asn Asn Phe Asn Lys Cys Thr Asn Asn Phe Asn Asn Ala Lys Asn His Ile Lys His Asn Ile Asn Asn Thr Asn Lys Asn Ile Glu His Leu Asn Asn His Ser 440 Ile Tyr Asn Phe Val Tyr Pro Glu Asn Lys Asn Ile Tyr Asp Ala Asn 455 Gly Asn Leu Ile Asn Asn Asn Ile Ser Tyr Thr Gln Leu Lys Met Asn 475 470 Asn Asn Ile Asn Phe Asn Ile His Met Glu Ser Pro Ile Asn Gln Gln 490 485 His Asn Asn Thr Phe Lys Val Asn Asn Asp Thr Asn Phe Phe Asn Glu 500 505 Pro Thr Asn Lys Met Lys Lys Lys Asn Lys Glu Lys Lys Asn Ile His Phe Asn Asn Asn Asn Asn Asn Asn Asn Lys Cys Leu Tyr Lys Asp 535 Ile Asn Gln Asn Asp His Asn Asn Ser Ile Ile Asn Thr Asn Gln Asn 550 555 545 Phe Asp His Ile Asn Asn Val Lys Asn Thr Glu Gln Asn Leu Gln Lys 570 Lys His Asn Lys Met Ser Gln Val Ser Lys Gln Ser Asn Asn Lys Asn 580 585 Asn Lys Asn Asn Ser His Leu Lys Lys Gln Ile Asn Ile Asn Thr Asn 600 595 Asn Asn Met Asp Asn Lys Asn Asn Ser His Ile Ser Lys Asn Val Ile 615 Val Asp Asp Asn Lys Leu Lys Ser Ser His Ala Asp Asn Ser Asn Glu

630

635

Ile Val Thr Lys Gly Lys Lys Lys Lys Asn Thr Asn Lys Lys Lys 645 Ile Asn Asn Ile Asn Ser Val Asn Asn Val Asn Asn Ile Asn Ser Met 665 660 Asn Asn Ile Asn Ser Met Asn Asn Ile Ile Ser Met Asn Asn Val Asn 680 Asn Met Asn Asn Pro Met Tyr Phe Pro Asn Val Asn Ile Gln Lys Asp 695 690 Asp Ser Asn Ile Ala Leu Leu Tyr Asn Asn Lys Pro Asn Ile Asp Phe 710 Asn Asn Phe Gln Leu Asn His Ile Asn Asn His Met Ile Gln Asn Asn 725 730 Ile Met Thr Asn Asn Val Met Leu Asn Asn Asn Leu Thr Thr Ser Asn Phe Asn Tyr Asn Leu Ile Asn Tyr Ser Tyr Glu Pro Phe Tyr Glu Glu Asn Leu Met Asn Asp Leu Asp Tyr Cys Arg Asp Ile Ser Leu Tyr Glu 770 775 Lys Arg Tyr Asp Arg Gly Asp Asn Leu Gln Gln Asn His Lys Arg Tyr 795 Asp Ile Asp Phe Pro Ser Leu 805 <210> 109 <211> 861 <212> PRT <213> Plasmodium falciparum <220> <221> misc\_feature

<223> hypothetical protein

<220>

<221> misc\_feature

<223> qi 4493994

<400> 109

Met Tyr Glu Leu Leu Leu Arg Phe Leu Lys Tyr Glu Cys Asp Tyr

Asp Asp Ser Glu Asp Ile Leu Asn Lys Tyr Cys Phe Ile Arg Glu Arg 20

Lys Tyr Asn Lys Pro Gly Gly Asn Lys Tyr Ile Pro Arg Asp Arg Ser 35 40 45

Asn Asn Asn Asn Ile Gly Asn Asn Val Asn Gly Met Asn Asn Phe 50 55 60

Val Leu Leu Asn Asn Asn Asn Asn Asn Met Arg Ile Arg Asn Thr Tyr 65 70 75 80

Asn Phe Asn Asn Phe Asn Asn Asn Asn Asn Asn Asn Asn Phe Asn Asn Asn 100 105 110

Phe Asn Asn Phe Asn Asn Asn Asn Phe Asn Asn Asn Asn His Phe 115 120 125

Asn Ile His Asn Ile Asp Asn Tyr Asp Asp Ser Tyr Val Lys Gly Arg 130 135 140

His Arg Gly Asn Tyr Leu Ser Ser Leu Asn Asn Ile Asn Gly Lys 145 150 155 160

Val Phe Lys Asn Leu Asp Asp Asn Cys Tyr Asn Leu Pro Thr Asn Asn 165 170 175

Leu Tyr Ile Asp Lys Glu Gly Lys Met His Leu Thr Gly Lys Glu His
180 185 190

Tyr Asn Ala Ala Ser Ser Asn Glu Tyr Asn His Asn Asn Lys Asn Thr 195 200 205

Asn Asn Tyr Asn Asn Asn Ser Tyr Asn Asn Asn Asn Phe Cys Asn Asn 210 215 220

Asn Tyr Asn Asp Asn Asn Tyr Asn Asn Ser Asn Asn Lys Gly Met Gly 225 230 235 240

Asn Lys Tyr Glu Arg Ser Leu Asn Tyr Leu Lys Lys Glu His Asp Met 245 250 255

Val Asp Tyr Glu Tyr Asn Asn Lys Gly Asn Ile Arg Lys Asn Asp Ser 260 265 270

Glu Lys Tyr Trp Asp Asn Pro Pro Leu His Tyr Ser Lys Lys Asn Asn 275 280 285

Tyr Asp Ile Phe Thr Leu Gly Asp Ile Lys Lys Tyr Ala Lys Asn Asn 290 295 300

Glu Lys Lys Gly Asn Asn Lys Tyr Met Asn Met His Asp Asn Asn Ser 305 310 315 320

Asn Asn Ser Asn Asn Val Leu Asn Asn Asn Met Asn Ser Asn Ser Asn Asn Tyr Asn Asn Ile Phe Lys Asp Asn Asp Glu Glu Asn Leu Thr 345 Lys Ser Asn Phe Ala Lys Trp Phe Lys Asn Asn Asn Met Asn Val 360 Asn Glu Asn Thr Asp Ile Ile Lys Tyr Leu Asn Asn Lys Asn Ser Gln 375 Gly His Ser Asp Gly Lys Asn Asn Asn Asn Asn Gly Asn Asn Ile 390 395 Ile Asn Asn Asn Ser Asn Asn Lys Asn Asn Ile Phe Gln Gly Asn Ser 410 Arg Asn Tyr Glu Asn Val Met Tyr Asn Ile Asn Asn Asn Asn Asn Asn Asn Ile Ile Ser Asn Asn Lys Asn Glu Ala Ser Phe Asn Thr Asp Asn 440 Ile Asn Thr Asn Ser Gly Arg Glu Glu Glu Lys Ile Ser Asn Thr Val 450 Ala Glu Leu Leu Met Lys Gln Ile Ser Met Ile Lys Glu Arg Asn Lys 470 Gly Leu Asp Val Leu Glu Lys Lys Asn Thr Phe Gly Phe Leu Asp Asn 490 Asn Tyr Gln Asn Tyr Gly Ser Asn Asn Ser Ser Leu Glu Lys Asn 505 Asn Met Lys Glu Asn Asp Ile Tyr Ser Lys Glu Ala Ser Lys Arg Ile 520 Met Asp Ile Phe Arg Thr Leu Asn Ser Asn Gly Leu Val Ser Gln Glu 535 530 Ser Leu Leu Val Asn Gln Ser Val Leu Asn Asn Asn Asn Asn Tyr Asn Asn Tyr Asn Ser Asn Asn Asn Arg Asn Lys Asn Gln Asn Asn Asn Asn Asn Asn Asn Asn Met Asn Asn Met Asn Asn Ser Asn Asn Asn Ile 580 Asn Asn Asn Asn Tyr Tyr Lys Asn Asn His Lys Tyr His Ser Met 600 Asp Asn Val Thr Tyr Lys Lys Ile Phe Ile Asn Asn Tyr Ser Asn Asn 610 615 , 620

Asp Gly Asn Asn Asn Ser Asn Asn Ser Asn Ser Asn Asn Asn Val Glu 625 630 635 640

His Tyr Tyr Met Asn Asn Lys Lys Asn Phe Lys Asn Lys Ile Asn Asn 645 650 655

Tyr His Asn Leu Pro Asp Asn Lys Asn Asn Met Met Asn Asn Asn Thr 660 665 670

Tyr Asn Asn Ile Asn Lys Asn Asn Leu Ser Asn Met Glu Asn Phe Pro 675 680 685

Pro Ser Leu Ser Phe Asn Asn Ser Asp Ile Asn Lys Asn Asn Ala Gln 690 695 700

Gly Asn Ile Asn Ile Thr Pro Ile Ile Asn Ser Ile Leu Arg Leu Asp 705 710 715 720

Asn Glu Val Asp Asn Val His Asn Asn Ser Ile Ser Glu Asn Ile Gln
725 730 735

Asn Ala Lys Val Ser Asn Val Leu Asp Ser Leu Lys Ser Leu Lys 740 745 750

Ala Ser Lys Ser Gln Gly Asn Asn Asn Tyr Asn Ile Pro Lys Asn Phe
755 760 765

Asn Asn Asn Asn Asn Asn Asn Asn Ser Lys Phe Ile Asn Tyr Asn 770 775 780

Ser Gln Gln Tyr Tyr Pro Ser His Gln Gln Gln Gln Gln Gln His Gln 785 790 795 800

Gln Gln Gln Gln Gln Gln Gln Gln Thr Leu Ile Gln Thr Gln Ile 805 810 815

Asn Ser Thr His Leu Asn Asp Phe Asn Lys Lys Lys Phe Asn Lys Lys 820 825 830

Glu Arg Tyr Pro Met Lys Tyr Pro Glu Phe Asp Gly Thr Thr Asn Glu 835 840 845

Thr Met Met Val Arg Glu Lys Ala Glu Arg Gln Leu Val 850 855 860

<210> 110

<211> 54

<212> PRT

<213> Plasmodium falciparum

<220>

<221> misc feature

<223> Homologue of C.elegans F49C12.11 protein

```
<220>
<221> misc_feature
<223> gi|4494004
<400> 110
Met Pro Leu Asn Thr Gln Gly Gly Lys Lys Pro Leu Lys Ala Ala
Lys Lys Gly Pro Val Glu Leu Thr Glu Glu Asp Ile Ala Phe Lys Lys
                               25
Glu Met Ala Glu Lys Lys Lys Ala Glu Glu Glu Ala Lys Gln Lys Leu
                           40
Leu Lys Ala Lys Lys
   50
<210> 111
<211> 71
<212> PRT
<213> L. major
<220>
<221> misc feature
<223> hypothetical protein P1105.01
<220>
<221> misc_feature
<223> gi 6996498
<400> 111
Met Arg Glu Arg Leu Ser Thr Asp Glu Tyr Val Tyr Trp Ser Gly Ile
Leu Leu Pro Leu Ile Arg Val Ile Asp Leu Ala Ser Val Asp Ser Pro
Leu Ala Leu Ala Leu Arg Ala Cys Val Cys Val Cys Val Cys
Val Cys Val Cys Val Cys Val Val Val Phe Leu Pro Leu Pro
Ser Leu Arg Ala Gln Ser Pro
65
<210> 112
<211> 923
```

```
<212> PRT
<213> L. major
<220>
<221> misc feature
<223> AC005941_2 L5204.2
<220>
<221> misc feature
<223> gi|6978417
<400> 112
Met Gln Leu Ser Gln Glu Asp Glu Glu Ala Ile Arg Thr Leu Arg Gly
Glu Ile Glu Ala Ala Trp Ala Lys Ala Asp Thr Ala His Glu Glu Glu
Gln Arg Ser Arg Glu Leu Leu His Thr Leu Arg Gln Gln Val Thr Glu
Leu Asp Ala Met Val Glu Lys Thr Ala Gly Leu Ser Met Gly Gln Glu
Ala Tyr Leu Arg Asp Leu Leu Thr Val Lys Lys Asp Arg Glu Glu
Ala Met Leu Leu His Ala Ala Leu Asn Arg Thr Glu Ala Asp His Arg
Gln Val Cys Val Gln Leu Ala Ala Lys Gln Ala His Glu Ala Ala
Gln Arg Glu Arg Asp Glu Gln Arg Gln Val Tyr Gln His Leu Leu Thr
                            120
Ser Leu Glu Ala Glu Gln Arg Glu Arg Ala Ala Lys Glu Ala Ser Val
    130
Arg Gln Tyr Arg Asp Thr Thr Glu Leu Cys Met Arg Arg Leu Asp Glu
Arg Gly Val Glu Val Glu Arg Ala Ile Arg Glu Glu Lys Lys Ala Ala
                                    170
Lys Glu Ala Glu Gly Thr Ala Gln Glu Ile Gln Ala Ile Ala Arg Gln
Leu Gln Glu Arg Gln Glu Arg Phe Gly Val Glu Ala Ala Arg Leu Ala
                            200
Ala Ala Glu Arg Glu Asn Thr Ile Leu Thr Arg Glu Leu Pro Gln Arg
```

210 215 220

Gln Al	a Ala	Leu	His	Glu	${\tt Gln}$	Gln	Asp	Glu	Leu	Lys	Arg	Glu	Glu	Lys
225				230					235					240

- Gln Leu His Leu Leu Glu Lys Ser Ala Arg Ala Gln Gln Ala Glu Leu 245 250 255
- Ala Ala Leu Val Glu Lys Arg Ala Thr Ala Ala Ala Ala Val Gln Thr
  260 265 270
- Arg Ala Asn Ser Val Asp Ala Ala Leu Thr Glu Leu Ala Thr Glu Glu
  275 280 285
- Lys Ala Arg Ala Ala Leu Glu Glu Ala Val Ala Lys Glu Met Gln Arg 290 295 300
- Lys Thr Asn Thr Met His Thr Asn Thr Phe Lys Ala Thr Ala Ser Ser 305 310 315 320
- Lys Val Glu Gly Gln Arg Val Met Glu Ala Gly Lys Ser Arg Arg Leu 325 330 335
- His Gln Gln Leu Glu Leu Leu Arg Thr Glu Asn Glu Lys Met Arg Lys 340 345 350
- Glu Ile Tyr Tyr Ala Glu Gln Asn His Glu Lys Asn Thr Lys Glu Ala 355 360 365
- Gln Gln Ala Leu Leu Asn Tyr His Arg Thr Leu Asp Ala Ile Arg Thr
- Arg Arg Ser Glu Ala Lys Ala Val Glu Glu Asp Ile Ala Leu His Gln 385 390 395 400
- Lys Lys Leu Lys Ala Gln Gln Ala Leu Leu Ser Thr Val Thr Ala Asp 405 410 415
- Arg Gln Lys Thr Glu Lys Ala Leu Arg Glu Thr Glu Ala Glu Leu Leu 420 425 430
- Leu Leu Arg Asn Arg His Ala Ser Lys Gln Glu Glu Leu Glu Ser Val 435 440 445
- Lys Thr Glu Leu Ile Gln Gln Glu Ala Asp Met Cys Gln Leu His Gly 450 455 460
- Leu Ser Arg Gln Leu Asn Lys Asp Val Ala Asn Thr Glu Gln Arg Leu 465 470 475 480
- Arg Phe Leu Arg Glu Asp Gln Gln His Ala Glu Ser Arg Val Glu Ala
  485 490 495
- Leu Arg Ser Glu Ala Gln Glu Leu Arg Gln Val Ile Ala Gln Tyr Asp 500 505 510

Leu Glu Ala Gln Gln Gln Gly Thr Arg Leu Lys Tyr Met Thr His Glu 515 520 525

Arg Asn Ala Ile Ala Thr Gln Leu Leu Arg Ser Glu Glu Leu Glu 530 535 540

Leu Ile Arg Glu Lys Ile Arg Leu Ala Asp Ala Thr Arg Val Ser Gly 545 550 555 560

Thr Thr Lys Tyr Gln Arg Ala Met Lys Gln Leu Leu Glu Ser Arg Asp 565 570 575

Leu Leu Val Glu Gln Arg Leu Arg Cys Arg Ile Ala Leu Val Arg Leu 580 585 590

Arg Tyr Leu Asp Arg Leu His Thr Lys Glu Val His Gln Glu Lys Leu 595 600 605

Leu Ser Gln Ser Arg Ala Arg Val Arg Ala Leu Ala Asp Glu Leu Gly 610 615 620

Thr Lys His Asn Val His Cys Trp Arg Ser Met Glu Ser Asn Ala Pro 625 630 635 640

Glu Val Leu Asp Ala Leu Ala Lys Val Gln Leu Leu Gln Ala Lys Leu 645 650 655

Leu Arg Lys His Gly Glu Leu Lys Glu Lys Thr Asp Leu Val Glu Lys 660 665 670

Glu Glu Arg Ala Tyr Gln Gln Leu Arg Gln Lys Leu Ala Arg Met Pro 675 680 685

Gly Pro Glu Ala Ala Glu Glu Leu Ala Leu Cys Ala Glu Asn Met Gln 690 695 700

Gln Arg Lys Ala Gln Leu Leu Cys Met Thr Asp Ser Leu Ala Glu Ala 705 710 715 720

Glu Gln Glu Ala Glu Val Leu Glu Val His Val Ala Gln Leu Gln Glu
725 730 735

Glu Leu Gln Asp Leu Lys His Arg Tyr Tyr Gln Glu Lys Thr Lys His 740 745 750

Ala Ala Leu Arg Gln Glu Glu Lys Leu Val Ala Arg Thr Trp Gly Ala 755 760 765

Gly Gly Ala Gly Ala Ala Arg Gln Ala Gly Ser Gly Thr Gly Ser Ser 770 780

Val Gly Asp Gly Asp Gly Ala Val Val Ala Ala Gly Ala Ser Ala Pro 785 790 795 800

Ser Ala Glu Gln Arg Arg Thr Asn Thr Asp Asp Arg Ser Pro Ser Ala Gly Gly Pro Ala Ser Ala Asp Val Glu His Arg Ser Ala Ser Gln Pro 825 Gln Gln Pro His Ser His Ala Gly Gly Ser Ala Ile Val Ser Asn Ser His Asn Gly Val Gln Ala Ala Ser Gly Thr Gly Arg Met Ser Ala 855 Ala Asn Ser Gly Arg Val Gly Asn Gly Ser Val Pro Pro Arg Asn Gly 870 875 Arg Arg Arg Ala Pro Leu Ala Glu Ala Ile Leu Asp Thr Leu Thr Ala 890 Gly Pro Pro Gln Pro Asn Phe Pro Leu Gln Arg Pro Pro His Gln Arg 905 Gln Phe Val Gly Gly Phe Ser Leu Thr Arg 920 <210> 113 <211> 2354 <212> PRT <213> L. major <220> <221> misc feature <223> AC005802\_5 L6202.3

<220>

<221> misc\_feature

<223> gi | 6899670

<400> 113

Met Ser Thr Pro Val Ser Gly Val Val Pro Gln Asp Arg Trp Gln Pro 1 5 10 15

Gln Gln Arg Val Lys Val Cys Gln Tyr Gln Asp Cys Gly Ala Pro Phe 20 25 30

Gly Phe Phe Ser Thr Lys Val Asn Cys His Arg Cys Gly Ile Val Leu 35 40 45

Cys Ser Lys Cys Ala Ala Thr Lys Thr Val Ile Pro Arg Tyr Tyr Ser 50 60

Asn Glu Thr Val Pro Val Cys Gln Arg Cys Tyr Gln Val Val Glu Arg 65 70 75 80

Tyr Lys Glu Arg Gly Ser Val Thr Pro Gly Tyr Val Val His Ser Thr 85 90 95

Thr Ile Ser Ala Thr Pro Ala Arg Ser Ser Pro Val Pro Pro Leu His
100 105 110

Thr Thr Pro Ala Leu Arg Pro His Ala Pro Ser Pro Gln Pro Ala Ser 115 120 125

Val Val Ser Thr Ala Thr Leu Val His Pro Val Glu Glu Asp Ala Val 130 135 140

Ser Thr Lys Pro Ser Val Ser Glu Ala Asp Leu His Ala Leu Arg Ser 145 150 155 160

Ile Ile Glu Thr Leu Gln Gln Ala Leu Asn Asp Glu Gln His Asn Ala 165 170 175

Ala Leu Ala Ala Thr Ser Ala Ala Glu Gln Leu Arg Thr Ala Lys Glu 180 185 190

Glu Asn Thr Ala Leu Lys Ser Thr Ala His Leu Leu Gln Gln Arg Leu 195 200 205

Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg 210 215 220

Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala 225 230 235 240

Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu 245 250 255

Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg 260 265 270

Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr 275 280 285

Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala 290 295 300

Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu 305 310 315 320

Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu 325 330 335

Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln 340 345 350

Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr 355 360 365

- Gln Gln Arq Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp 370 Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln 390 Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln 410 Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp 425 Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu 440 Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu 450 Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu 470 475 Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln 490 Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala 500 Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala 520 Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg 540 Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu 550 Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu 570 Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 580 Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr 600
- Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Val Asp 610 615 620
- Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln 625 630 635 640
- Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln
  645 650 655
- Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala

660 665 670

Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln 675 680 685

Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp 690 695 700

Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg 705 710 715 720

Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala
725 730 735

Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn 740 745 750

Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala 755 760 765

Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala
770 780

Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp
785 790 795 800

Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu 805 810 815

Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu 820 825 830

Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu 835 840 845

Glu Ala Gln Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln 850 855 860

Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala 865 870 875 880

Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala 885 890 895

Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg 900 905 910

Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu 915 920 925

Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu 930 935 940

Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg 945 950 955 960 Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala 965 970 975

Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu 980 985 990

Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg 995 1000 1005

Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp 1010 1015 1020

Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 1025 1030 1035

Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn 1040 1045 1050

Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg 1055 1060 1065

Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp 1070 1075 1080

Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 1085 1090 1095

Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln 1100 1105 1110

Val Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu 1115 1120 1125

Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr 1130 1135 1140

Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala 1145 1150 1155

Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu 1160 1165 1170

Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu 1175 1180 1185

Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg 1190 1195 1200

Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp 1205 1210 1215

Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 1220 1225 1230 Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn 1240 1235 Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg 1255 Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp 1270 Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 1290 1285 Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln 1300 Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu 1310 1315 Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala 1330 1325 Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala 1345 1340 Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln 1360 1355 Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg 1370 1375 Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln 1390 1395 1385 Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala 1410 1405 1400 Gln Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg 1420 Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val 1435 1430 Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala 1450 1445 Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln 1465 1470 Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala Asp 1475 1480 Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu 1495 Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu

1510 , 1515 Ala Arg Val Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Val Glu Met Ala Val Leu Leu Arg Glu Arg Glu Glu Ala Arg Gly Glu Thr Ala Val Ala Gly Glu Gln Val Gln Leu Tyr Arg Glu Thr Val Glu Glu Glu Cys 

Leu Lys Glu Glu Arg Trp Cys Leu Glu Ser Arg Val Ala Gln Leu 1795 1790 Arg Glu Ala Ser Ala Ala Ala Lys Gln Gln Arg Gln Glu Val Ala 1810 1815 1805 Ala Lys Ala Asn Glu Val Gln Glu Arg Leu Asp Ser Met Ala Arg 1830 1825 1820 Arg Cys Ile Ala His Glu Gly Asp Ala Pro Gln Arg Ala Asp Gly 1840 Arg Asp Asp Ala Leu Arg Gln Leu Ala Asn Leu Arg Glu Glu Val 1855 1850 Lys Leu Ser Glu Lys Gln Lys Ala Met Glu Arg Val Ile Pro Gly 1865 1870 Val Arg Glu Arg Gln Met Arg Leu Glu Ala Ala Glu Glu Gln Arg 1885 Ala Asp Leu Glu Ala Arg Leu Val Asp Glu Ala Gly Asp Leu Arg 1905 1900 1895 Ser Arg Pro Ala Ala Ser Thr Asn Glu Val Asn Leu Tyr Arg Asp 1915 Leu Ala Leu Gln Glu His Glu Ala Ala Gln Asn Arg Cys Thr Thr 1930 1925 Leu Glu Ala Gln Val Ala Ser Leu Thr Ser Asp Arg Asp Asn Gly 1945 1950 1940 Arg Gln Glu Ser Ala Asp Leu Ser Glu Ala Gln Arg His Leu 1960 Asp Asn Val Gln Glu Arg Asp Met Ala His His Arg Cys Ala Ala 1980 1975 1970 Leu Glu Glu Gln Asn Ala Ala Met Ala Ser Glu Leu Gln Ala Val 1990 Lys Ala Lys Leu Arg Gln Ala Ser Val Lys Ala Ser Ser Leu Met 2005 2000 Thr Arg Leu Ser Ala Ser Ser Ser Gly Ala Gly Gly Val Ser Ala 2020 2015 Arg Val Arg Val Gly Gly Ser Ser Ala Val Pro Gln Ala Ala Pro 2035 His Arg Asp Ala Glu Leu Ile Ala Glu Val Gly Glu Arg Leu Arg 2055 2050 2045

Glu Arg Gly Glu Ala Met Arg Leu Leu Ala Glu Gly Val Glu Leu 2065 2060 Arg Glu Arg Ala Arg Pro Leu Glu Arg Val Leu Ala Glu Lys Leu 2080 Ile Gly Asp Arg Arg Thr Ser Asp Ala Glu Glu Val Ala Thr Glu 2095 Pro Thr Gln Val Arg Arg Asn Ala Ala His Ser Arg His Leu Asp 2115 2110 Ser Arg Glu Ala Gln Leu Asp Glu Arg Ala Ala Arg Leu Arg Glu 2125 Lys Glu Gln Gln Leu Leu Arg Val Ala Arg Glu Leu Gln Thr Lys 2135 2140 Ser Arg Ala Leu Gln Val Leu Tyr Ala Arg Ala Leu Asn Arg Pro 2155 2150 Gln Val Thr Ser Leu Leu Leu Thr Ala Asp Gly Asp Asp Thr Ser 2170 2165 Tyr Pro Asp Thr Pro Gln Gln Gln Gln Gly Thr Arg Thr Pro 2185 2190 2180 Leu Arg Glu Pro Val Tyr Ser Leu Asp Ser Glu Val Ala His Tyr 2195 2200 Gly Arg Thr Ala Gly Ala Ala Val Ser Ser Gly Leu Ala Ser Pro 2215 2210 Leu Pro Arg Glu Pro Pro Arg Ala Arg Met Val His Arg Ala Val 2230 2225 Glu Ala Thr Gly Thr Glu Glu Asp Thr Gln Val Arg Leu Thr Ala 2245 Ala Thr Glu Ala Tyr Arg Asp Val Leu Tyr Glu His Ile Leu Glu 2260 2255 Ser Asn Gly Leu Gln Gly Val Asp Val Leu Ala Gln Tyr Leu Pro 2270 His His Thr Ser Gly Gly Gly Leu Lys Thr Pro Arg Leu Pro Gly 2295 2290 2285 Ser Gly Ile Ile Ser Lys Thr Arg Ala Met Leu Arg Ala Leu Glu 2310 2300 2305 Glu Arg Leu Gly Ala Ser Arg Gly Val Gly Arg Gly Val Asp Pro 2320 Ala Val Gln Glu Arg Ser Leu Glu Ala Phe Arg Arg Leu Glu Ala 2330 2335 2340

Ala Leu Ser Ala Leu Cys Gly Gly Ser His Ala 2345 2350

<210> 114

<211> 2310

<212> PRT

<213> L. major

<220>

<221> misc\_feature

<223> AC005893\_12 L6202.3

<220>

<221> misc\_feature

<223> gi|6899664

<400> 114

Met Ser Thr Pro Val Ser Gly Val Val Pro Gln Asp Arg Trp Gln Pro 1 5 10 15

Gln Gln Arg Val Lys Val Cys Gln Tyr Gln Asp Cys Gly Ala Pro Phe 20 25 30

Gly Phe Phe Ser Thr Lys Val Asn Cys His Arg Cys Gly Ile Val Leu 35 40 45

Cys Ser Lys Cys Ala Ala Thr Lys Thr Val Ile Pro Arg Tyr Tyr Ser

Asn Glu Thr Val Pro Val Cys Gln Arg Cys Tyr Gln Val Val Glu Arg 65 70 75 80

Tyr Lys Glu Arg Gly Ser Val Thr Pro Gly Tyr Val Val His Ser Thr
85 90 95

Thr Ile Ser Ala Thr Pro Ala Arg Ser Ser Pro Val Pro Pro Leu His 100 105 110

Thr Thr Pro Ala Leu Arg Pro His Ala Pro Ser Pro Gln Pro Ala Ser 115 120 125

Val Val Ser Thr Ala Thr Leu Val His Pro Val Glu Glu Asp Ala Val 130 135 140

Ser Thr Lys Pro Ser Val Ser Glu Ala Asp Leu His Ala Leu Arg Ser 145 150 155 160

Ile Ile Glu Thr Leu Gln Gln Ala Leu Asn Asp Glu Gln His Asn Ala 165 170 175

- Ala Leu Ala Ala Thr Ser Ala Ala Glu Gln Leu Arg Thr Ala Lys Glu 180 185 190
- Glu Asn Thr Ala Leu Lys Ser Thr Ala His Leu Leu Gln Gln Arg Leu 195 200 205
- Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 210 215 220
- Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala 225 230 235 240
- Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu 245 250 255
- Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg 260 265 270
- Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr 275 280 285
- Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala 290 295 300
- Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln 305 310 315 320
- Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp 325 330 335
- Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg 340 345 350
- Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala 355 360 365
- Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala 370 375 380
- Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala 385 390 395 400
- Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu
  405 410 415
- Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala 420 425 430
- Gln Val Ala Arg Leu Ala Ala Asn Arg Asp Glu Ala Arg Gln Gln Leu 435 440 445
- Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln 450 455 460
- Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala Asp Arg

465 470 ' 475 480

Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 485 490 495

Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val
500 505 510

Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala 515 520 525

Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg
530 540

Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asn Ala Glu Glu 545 550 555 560

Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu
565 570 575

Ala Gln Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg 580 585 590

Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala 595 600 605

Arg Leu Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn 610 615 620

Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala 625 630 635 640

Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala 645 650 655

Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp
660 665 670

Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu 675 680 685

Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu 690 695 700

Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu 705 710 715 720

Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln
725 730 735

Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala
740 745 750

Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala 755 760 765

- Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu
  770 775 780
- Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala
  785 790 795 800
- Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu
  805 810 810
- Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln 820 825 830
- Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Gly 835 840 845
- Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 850 855 860
- Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val 865 870 875 880
- Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala 885 890 895
- Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg
  900 905 910
- Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu 915 920 925
- Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu 930 940
- Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 945 950 955 960
- Leu Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala 965 970 975
- Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu 980 985 990
- Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg 995 1000 1005
- Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp 1010 1015 1020
- Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg 1025 1030 1035
- Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala 1040 1045 1050

Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp

1330 , 1335 1325 Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu 1345 1350 Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu 1355 1360 Ala Gln Val Ala Arg Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 1370 Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg 1385 1390 Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu 1405 Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr 1415 1420 Gln Gln Arg Ala Glu Leu Glu Ala Gln Val Ala Arg Leu Ala Ala 1430 1435 Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu 1450 Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu 1460 1465 Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg 1480 Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp 1490 1495 Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg 1505 1510 Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn 1525 Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg 1535 1540 Ala Glu Leu Glu Ala Arg Val Ala Arg Leu Ala Ala Asp Gly Asp 1555 1560 Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln 1565 1570 1575 Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Arg 1580 1585 Val Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu 1595 1600

Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Arg Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Ala Gln Leu Ala Arg Leu Ala Ala Asp Gly Asp Glu Ala Arg Gln Gln Leu Ala Ala Asn Ala Glu Glu Leu Gln Gln Arg Leu Asp Thr Ala Thr Gln Gln Arg Ala Glu Leu Glu Val Glu Met Ala Val Leu Leu Arg Glu Arg Glu Glu Ala Arg Gly Glu Thr Ala Val Ala Gly Glu Gln Val Gln Leu Tyr Arg Glu Thr Val Glu Glu Glu Cys Leu Lys Glu Glu Arg Trp Cys Leu Glu Ser Arg Val Ala Gln Leu Arg Glu Ala Ser Ala Ala Ala Lys Gln Gln Arg Gln Glu Val Ala Ala Lys Ala Asn Glu Val Gln Glu Arg Leu Asp Ser Met Ala Arg Arg Cys Ile Ala His Glu Gly Asp Ala Pro Gln Arg Ala Asp Gly Arg Asp Asp Ala Leu Arg Gln Leu Ala Asn Leu Arg Glu Glu Val Lys Leu Ser Glu Lys Gln Lys Ala Met Glu Arg Val Ile Pro Gly Val Arg Glu Arg Gln Met Arg Leu Glu Ala Ala Glu Glu Gln Arg Ala Asp Leu Glu Ala Arg Leu Val Asp Glu Ala Gly Asp Leu Arg Ser Arg Pro Ala Ala Ser Thr Asn Glu Val Asn Leu Tyr Arg

Asp Leu Ala Leu Gln Glu His Glu Ala Ala Gln Asn Arg Cys Thr 1880 1885 Thr Leu Glu Ala Gln Val Ala Ser Leu Thr Ser Asp Arg Asp Asn 1900 Gly Arg Gln Gln Glu Ser Ala Asp Leu Ser Glu Ala Gln Arg His 1910 1915 Leu Asp Asn Val Gln Glu Arg Asp Met Ala His His Arg Cys Ala 1930 1935 Ala Leu Glu Glu Gln Asn Ala Ala Met Ala Ser Glu Leu Gln Ala 1940 1945 Val Lys Ala Lys Leu Arg Gln Ala Ser Val Lys Ala Ser Ser Leu 1955 1960 1965 Met Thr Arg Leu Ser Ala Ser Ser Ser Gly Ala Gly Gly Val Ser 1970 Ala Arg Val Arg Val Gly Gly Ser Ser Ala Val Pro Gln Ala Ala 1985 1990 Pro His Arg Asp Ala Glu Leu Ile Ala Glu Val Gly Glu Arg Leu 2000 2005 Arg Glu Arg Gly Glu Ala Met Arg Leu Leu Ala Glu Gly Val Glu 2020 Leu Arg Glu Arg Ala Arg Pro Leu Glu Arg Val Leu Ala Glu Lys 2030 2035 Leu Ile Gly Asp Arg Arg Thr Ser Asp Ala Glu Glu Val Ala Thr 2045 2050 Glu Pro Thr Gln Val Arg Arg Asn Ala Ala His Ser Arg His Leu 2060 2065 Asp Ser Arg Glu Ala Gln Leu Asp Glu Arg Ala Ala Arg Leu Arg 2075 2080 Glu Lys Glu Gln Gln Leu Leu Arg Val Ala Arg Glu Leu Gln Thr 2095 Lys Ser Arg Ala Leu Gln Val Leu Tyr Ala Arg Ala Leu Asn Arg 2105 2110 Pro Gln Val Thr Ser Leu Leu Leu Thr Ala Asp Gly Asp Asp Thr 2120 2125 Ser Tyr Pro Asp Thr Pro Gln Gln Gln Gln Gln Gly Thr Arg Thr 2140 Pro Leu Arg Glu Pro Val Tyr Ser Leu Asp Ser Glu Val Ala His

2155 , , 2150 2160 Tyr Gly Arg Thr Ala Gly Ala Ala Val Ser Ser Gly Leu Ala Ser 2165 2170 2175 Pro Leu Pro Arg Glu Pro Pro Arg Ala Arg Met Val His Arg Ala 2180 Val Glu Ala Thr Gly Thr Glu Glu Asp Thr Gln Val Arg Leu Thr 2195 Ala Ala Thr Glu Ala Tyr Arg Asp Val Leu Tyr Glu His Ile Leu 2210 2215 Glu Ser Asn Gly Leu Gln Gly Val Asp Val Leu Ala Gln Tyr Leu 2230 Pro His His Thr Ser Gly Gly Leu Lys Thr Pro Arg Leu Pro 2240 2245 Gly Ser Gly Ile Ile Ser Lys Thr Arg Ala Met Leu Arg Ala Leu 2255 2260 Glu Glu Arg Leu Gly Ala Ser Arg Gly Val Gly Arg Gly Val Asp 2275 Pro Ala Val Gln Glu Arg Ser Leu Glu Ala Phe Arg Arg Leu Glu 2285 2290 Ala Ala Leu Ser Ala Leu Cys Gly Gly Ser His Ala 2300 2305 <210> 115 <211> 125 <212> PRT <213> L. major <220> <221> misc feature <223> hypothetical protein L7276.03 <220> <221> misc\_feature <223> gi | 6562665 <400> 115 Met Asn Ser Ala Asp Ala Leu Glu Pro Ile Pro Arg Ser Ile Ala Pro

Asp Gln Glu Leu Ser Ile Leu Lys Leu Ile Leu Asp Leu Arg Ser Leu

```
Gly Asp Val Glu Gly Ser Lys Lys Val Arg Arg Val Arg Glu Ala
Leu Leu Lys Ser Ser Asp Asp Ser Glu Ala Met Ser Lys Val Asp Asp
Ile Ile Arg Arg Gly Lys Arg Thr Gln Ser Lys Leu Asp Gly Ser Tyr
Asp Glu Arg Gln Arg Leu Lys Arg Lys Arg Arg Glu Glu Asp Leu Ala
Ala Ala Ser Arg Leu Val Asp Val Glu Ala Gly Ser Gly Glu Asp Ser
Glu Gly Ser Ala Ser Thr Glu Glu Asp Gly Thr Glu Asp
<210> 116
<211> 57
<212> PRT
<213> L. major
<220>
<221> misc_feature
<223> hypothetical protein P1105.12
<220>
<221> misc feature
<223> gi | 6996509
<400> 116
Gln Pro Asn Asp Leu Ile Glu Ala Leu Asn Gly Thr Arg Val Arg Asn
Val Gly Asp Phe Arg Arg Val Ile Glu Glu Glu Leu Thr Pro Gly Met
Ile Val Pro Val Arg Ile Asn Arg Gly Gly Val Ala Met Val Val Thr
Val Arg Val Glu Ala Gly Arg Ser Leu
                        55
<210> 117
<211> 94
<212> PRT
<213> L. major
<220>
<221> misc feature
```

<223> hypothetical protein L2743.10

```
<220>
 <221> misc_feature
<223> gi 6433946
<400> 117
Met Ile Ser Val Asp Leu His His His Lys Thr Arg Ile Glu Met His
Val Lys Ala Cys Asn Asp Arg Ser His Arg His Thr His Thr
                                25
His Thr Asn Ser Phe Val Ser Gly Asp Val Phe His Val Trp Arg Val
                            40
Arg Ser Phe His Ser Ala Pro Ser Val Phe Phe Cys Phe Ser Val Cys
Thr His Leu Leu Phe Ser Pro Ser Pro Tyr Ala His His Ala Arg
Val Cys Val Arg Ala Cys Val Cys Val Cys Val Cys Val Val
<210> 118
<211> 121
<212> PRT
<213> L. major
<220>
<221>
      misc_feature
<223> hypothetical protein L2719.11
<220>
<221> misc_feature
<223> gi|5869911
<400> 118
Met Ile Ser Leu Met Leu Leu Ala Ala Leu Leu Trp Gly Val Thr Asn
Pro Leu Leu Lys His Tyr Ser Arg Gly Met Ala Ser Ser Gly Ser Ala
                               25
Lys Asp Asp Ala Leu Phe Leu Val Arg Pro Lys Tyr Leu Val Ala
```

154/155

Gln Ala Val Asn Leu Ser Gly Ser Val Val Phe Phe His Ser Leu Arg

Glu Val Asp Val Ser Val Gly Ser Ile Val Val Asn Ser Leu Ala Phe 65 70 75 80

Val Ile Thr Val Leu Met Ser Val Leu Val Leu Arg Glu Gly Leu Leu 85 90 95

Arg Ala Arg Thr Thr Ala Gly Cys Leu Leu Val Met Val Gly Thr Ala 100 105 110

Leu Cys Thr Tyr Ser Ser Ser Ala Ser 115 120